

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 02:25:13 ; Search time 6630 Seconds
(without alignments)
2588.815 Million cell updates/sec

Title: US-09-684-215B-3
Perfect score: 396
Sequence: 1 acggccgcgcgcgataactt.....tggcccgaggagcccccgcc 396

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_bat.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pri.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
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32: em_htg_other.*
33: em_htg_mus.*
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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	396	100.0	702	6	BD251334	BD251334 Fused pro
2	396	100.0	702	6	AR403747	AR403747 Sequence
3	396	100.0	1068	6	BD274032	BD274032 Sequences
4	396	100.0	1068	6	AX005788	AX005788 Sequence
5	396	100.0	1143	6	BD274033	BD274033 Sequences
6	396	100.0	1143	6	AX005790	AX005790 Sequence
7	396	100.0	2287	6	BD251322	BD251322 Fused pro
8	396	100.0	2287	6	AR303127	AR303127 Sequence
9	396	100.0	2287	6	AR403735	AR403735 Sequence
10	396	100.0	14029	1	AE006925	AE006925 Mycobacte
11	396	100.0	341957	15	BX842572	BX842572 Mycobacte
12	396	100.0	343050	1	EX248334	EX248334 Mycobacte
13	394.4	99.6	447	6	AR169152	AR169152 Sequence
14	394.4	99.6	447	6	AR182442	AR182442 Sequence
15	394.4	99.6	447	6	AR194825	AR194825 Sequence
16	394.4	99.6	447	6	AR233097	AR233097 Sequence
17	394.4	99.6	447	6	AX353302	AX353302 Sequence
18	394.4	99.6	447	6	AX429596	AX429596 Sequence
19	394.4	99.6	447	6	AX832581	AX832581 Sequence
20	394.4	99.6	447	6	BD006325	BD006325 Compounds
21	394.4	99.6	447	6	BD006445	BD006445 Compounds
22	394.4	99.6	447	6	BD069285	BD069285 Compounds
23	394.4	99.6	447	6	BD205817	BD205817 Compounds
24	391.2	98.8	1872	6	AR189165	AR189165 Sequence
25	391.2	98.8	1872	6	AR182455	AR182455 Sequence
26	391.2	98.8	1872	6	AR194838	AR194838 Sequence
27	391.2	98.8	1872	6	AR233110	AR233110 Sequence
28	391.2	98.8	1872	6	AR353315	AR353315 Sequence
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35	354	89.4	675	6	AR261272	AR261272 Sequence
36	354	89.4	675	6	AR400535	AR400535 Sequence
37	354	89.4	675	6	AR405802	AR405802 Sequence
38	354	89.4	675	6	AX201049	AX201049 Sequence
39	354	89.4	675	6	AX267848	AX267848 Sequence
40	354	89.4	822	6	AR277645	AR277645 Sequence
41	354	89.4	894	6	AX369152	AX369152 Sequence
42	354	89.4	894	6	AX351489	AX351489 Sequence
43	354	89.4	900	6	AR220690	AR220690 Sequence
44	354	89.4	900	6	AX365960	AX365960 Sequence
45	354	89.4	915	6	AR261281	AR261281 Sequence

ALIGNMENTS

RESULT 1	BD251334	702 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD251334	Fused protein of Mycobacterium tuberculosis antigen and utilization thereof			
DEFINITION	BD251334				
ACCESSION	BD251334				
VERSION	BD251334.1	GI:33061104			
KEYWORDS	JP 2002510494-A/13.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 702)				
AUTHORS	Skeiky, Y.A.W., Alderson, M. and Neto, A.C.				
TITLE	Fused protein of Mycobacterium tuberculosis antigen and utilization thereof				

Pred. No. is the number of results predicted by chance to have a

PC C07K16/12,
PC C07K19/00,C12N1/21,C12P21/02,C12Q1/02,C12Q1/68,G01N33/50, PC
G01N33/53//
PC (C12N15/09,C12R1.32),C12N15/00,(C12N15/00,C12R1.32) CC 50D
FH Key Location/Qualifiers
FT CDS (1):..(1065).

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Best Local Similarity 100.0%; Pred. NO. 4.1e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 670 ACGGCCGCTCCGATACCTCCAGCTGTCCAGGTCGGGAGGATTCGCCATTCCGATC 729
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DB 730 GGGCAGCGATGGCGATCGGGGCGAGATCCGATCGGTCGGGGGTCAACCACCGTTTCA 789
QY 121 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACCAACACGCGACGACGA 180
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QY 301 GGGCATCATCCGCTGACGTCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGT 360
DB 970 GGGCATCATCCGCTGACGTCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGT 1029
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DB 1030 ACAGGAAACGTGACATTCGGCGGAGGACCCCGGCC 1065

RESULT 4
AX005788
LOCUS AX005788 1068 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 907 from Patent WO9909186.
ACCESSION AX005788
VERSION AX005788.1 GI:9928795
KEYWORDS
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.

REFERENCE
1. Portnoi,D. and Guigueno,A.
Polypeptide nucleic sequences exported from mycobacteria, vectors
comprising same and uses for diagnosing and preventing tuberculosis
Patent: WO 9909186-A 907 25-FEB-1999.
JOURNAL PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 396; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. NO. 4.1e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGGCCGCTCCGATACCTTCAGCTGTCCAGGTCGGGAGGATTCGCCATTCCGATC 60
DB 670 ACGGCCGCTCCGATACCTTCAGCTGTCCAGGTCGGGAGGATTCGCCATTCCGATC 729
QY 61 GGGCAGCGATGGCGATCGGGGCGAGATCCGATCGGTCGGGGGTCAACCACCGTTTCA 120
DB 730 GGGCAGCGATGGCGATCGGGGCGAGATCCGATCGGTCGGGGGTCAACCACCGTTTCA 789
QY 121 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACCAACACGCGACGACGA 180
DB 790 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACCAACACGCGACGACGA 849
QY 181 GTCCAAACGCTGTCGGAGCGCTCCGCGGCAAGTTCGGCATCTCCACCGCGACGTG 240
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QY 241 ATCCACCGGTCGACGGCTCCGATCACTCGGTCGACGCGGATGGCGGACGCGTTAAC 300
DB 910 ATCCACCGGTCGACGGCTCCGATCACTCGGTCGACGCGGATGGCGGACGCGTTAAC 969
QY 301 GGGCATCATCCGCTGACGTCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGT 360
DB 970 GGGCATCATCCGCTGACGTCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGT 1029
QY 361 ACAGGAAACGTGACATTCGGCGGAGGACCCCGGCC 396
DB 1030 ACAGGAAACGTGACATTCGGCGGAGGACCCCGGCC 1065

RESULT 5
BD274033
LOCUS BD274033 1143 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequences nucleic acid from polypeptides exportes from
mycobacteries, vector the complement and applications at diagnostic
and the prevention from the tuberculosis.

ACCESSION BD274033
VERSION BD274033.1 GI:33083801
KEYWORDS JP 2002534956-A/257.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.

REFERENCE
1. (bases 1 to 1143)
Gicquel,B., Portnoi,D., Lim,E., Pelicic,V., Guigueno,A. and
Salmoniere,Y.G.D.L.
Sequences nucleic acid from polypeptides exportes from
mycobacteries, vector the complement and applications at diagnostic
and the prevention from the tuberculosis
Patent: JP 2002534956-A 257 22-OCT-2002;
JOURNAL INSTITUT PASTEUR
COMMENT OS Mycobacterium tuberculosis
PN JP 2002534956-A/257
PD 22-OCT-2002
PF 14-AUG-1998 JP 2000509849
PR 14-AUG-1997 FR 97/10404,11-SEP-1997 FR 97/11325 PI
BRIGITTE GICQUEL,DENIS PORTNOI,ENG-MONG LIM,VLADIMIR PELICIC, PI

PC C12N15/00
CC Description of Artificial Sequence:tri-fusion protein Ra12- CC
TbH9-Ra35
CC (designated Mtb32A)
CC n = g, a, c or t
CC n = g, a, c or t
CC n = g, a, c or t
PH Key Location/Qualifiers
FT modified base (30)
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FT CDS (42).. (2231)
FT modified base (2270).
Location/Qualifiers
1. .2287
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FEATURES
source

ORIGIN

Query Match 100.0%; Score 396; DB 6; Length 2287;
Best Local Similarity 100.0%; Pred. No. 3.6e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 60
DB 63 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 122
QY 61 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 120
DB 123 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 182
QY 121 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGGACGCGCAGCA 180
DB 183 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGGACGCGCAGCA 242
QY 181 GTCCAAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGACGTG 240
DB 243 GTCCAAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGACGTG 302
QY 241 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC 300
DB 303 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC 362
QY 301 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
DB 363 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 422
QY 361 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 396
DB 423 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 458

RESULT 9
AR403735 2287 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6627198.
ACCESSION AR403735
VERSION AR403735.1 GI:40151411
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.
TITLE Fusion proteins of Mycobacterium tuberculosis antigens and their uses
JOURNAL Patent: US 6627198-A 1 30-SEP-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.6e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 60
DB 63 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 122
QY 61 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 120
DB 123 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 182
QY 121 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGGACGCGCAGCA 180
DB 183 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGGACGCGCAGCA 242
QY 181 GTCCAAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGACGTG 240
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QY 301 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
DB 363 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 422
QY 361 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 396
DB 423 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 458

RESULT 8
AR303127 2287 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 1 from patent US 6544522.
ACCESSION AR303127
VERSION AR303127.1 GI:31691855
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Skeiky,Y., Alderson,M. and Campos-Neto,A.
TITLE Fusion proteins of mycobacterium tuberculosis antigens and their uses
JOURNAL Patent: US 6544522-A 1 08-APR-2003;
FEATURES Location/Qualifiers
source 1. .2287
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Query Match 100.0%; Score 396; DB 6; Length 2287;
Best Local Similarity 100.0%; Pred. No. 3.6e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 60
DB 63 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 122
QY 61 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 120
DB 123 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 182
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QY 181 GTCCAAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGACGTG 240
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QY 241 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC 300
DB 303 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC 362
QY 301 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
DB 363 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 422
QY 361 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 396
DB 423 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 458

RESULT 9
AR403735 2287 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6627198.
ACCESSION AR403735
VERSION AR403735.1 GI:40151411
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.
TITLE Fusion proteins of Mycobacterium tuberculosis antigens and their uses
JOURNAL Patent: US 6627198-A 1 30-SEP-2003;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 396; DB 6; Length 2287;
Best Local Similarity 100.0%; Pred. No. 3.6e-57;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 60
DB 63 ACGCCCGCTCCGATACCTTCCAGCTCTCCAGGTCGGCAGGATTCGCCATTCCGATC 122
QY 61 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 120
DB 123 GGGCAGCGATGGCGATCGCGGCGCAGATCCGATCGGTCGGGGGTCAACCCACCGTTTCA 182
QY 121 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGGACGCGCAGCA 180
DB 183 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGGACGCGCAGCA 242
QY 181 GTCCAAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGACGTG 240
DB 243 GTCCAAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGACGTG 302
QY 241 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC 300
DB 303 ATCACCGCGTCGACGGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC 362
QY 301 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
DB 363 GGGCATCATCCCGTGGTGCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 422
QY 361 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 396
DB 423 ACAGGGAACGTGACATTCGGCGAGGACCCCGGCC 458

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Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 AC 297050;
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 SV EX842572.1
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 DT 21-NOV-2003 (Rel. 77, Created)
 DT 21-NOV-2003 (Rel. 77, Last updated, Version 1)
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 DE Mycobacterium tuberculosis H37Rv complete genome; segment 1/13
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 KW complete genome.
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 OS Mycobacterium tuberculosis H37Rv
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex; Mycobacterium tuberculosis.
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 [1]
 MEDLINE; 98295987.
 RX PUBMED; 9634230.
 RA Cole S.T., Brasch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eigemeier K., Gas S., Barry III C.E., Tekala F., Badcock K.,
 Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K.,
 Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornby T., Jagels K.,
 Krog A., McLean J., Moule S., Murphy L., Oliver S., Osborne J.,
 Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S.,
 Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the complete
 RT genome sequence";
 RL Nature 393:537-544 (1998).
 XX
 [2]
 RX PUBMED; 12368430.
 RN Camus J.C., Pryor M.J., Medigue C., Cole S.T.;
 RA "Re-annotation of the genome sequence of Mycobacterium tuberculosis H37Rv";
 RL Microbiology 148:2967-2973(2002).
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FT      /note="PS00618 RecF protein signature 2"
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FT      /note="Rv0004 (MTCV10H4.02), len: 187 aa. Conserved
FT      hypothetical protein (see Salazar et al., 1996), highly
FT      similar, but longer 21 aa in N-terminus, to
FT      AAF33696.1|AF222789 unknown protein from Mycobacterium
FT      avium subsp. paratuberculosis (166 aa); and highly similar
FT      to NP_301132.1|NC_002677 conserved hypothetical protein
FT      from Mycobacterium leprae (189 aa); S70990 hypothetical
FT      protein from Mycobacterium smegmatis (194 aa). Also highly
FT      similar, except in N-terminal part, to
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FT      BX248334 BX248333
FT      VERSION
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FT      Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
FT      tuberculosis complex.
FT
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FT      AUTHORS
FT      Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
FT      Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
FT      Harris B., Atkin R., Doggett J., Mayes R., Keating L.,
FT      Wheeler P.R., Farhrell J., Barrell B.G., Cole S.T., Gordon S.V. and
FT      Hewison G.
FT      The complete genome sequence of Mycobacterium bovis
FT      Online Publication
FT      PNAS 10.1073/pnas.1130426100 ( Microbiology )
FT      REFERENCE
FT      2 (bases 1 to 343050)
FT      AUTHORS
FT      Garnier T.
FT      TITLE
FT      Direct Submission
```

JOURNAL

Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire
Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex
15, France. e-mail:tgarnier@pasteur.fr Submitted on behalf of the
Mycobacterium bovis sequencing teams, TB Research Group, Veterinary
Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlestone,
Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK. PT4 Annotation, Genopole, Institut
Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France.
Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28
rue du Docteur Roux, 75724 Paris Cedex 15, France

FEATURES

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/strain="AF2122/97"
/db_xref="taxon:233413"

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CDS

1..1524
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(99.8% identity in 507 aa overlap). dnaA, chromosomal
replication initiator protein (see citations below).
equivalent to other Mycobacterial CHROMOSOMAL REPLICATION
INITIATOR PROTEINS e.g. P46388|DnaA_MYC from
Mycobacterium leprae (502 aa); Q9L7L7|DnaA_MYC from
Mycobacterium paratuberculosis (509 aa); P49992|DnaA_MYC from
from Mycobacterium avium (508 aa); P49992|DnaA_MYC from
Mycobacterium smegmatis (504 aa); etc. Also highly similar
to others except in N-terminus e.g. Q9ZH75|DnaA_STRCH
CHROMOSOMAL REPLICATION INITIATOR PROTEIN from
Streptomyces chrysomallus (624 aa); Q9ZH76|DnaA_STRCH from
Streptomyces reticuli (643 aa); DnaA_ECOLI|P03004|B3702
chromosomal replication initiator protein from Escherichia
coli strain K12 (467 aa), FASTA scores: opt: 986, E(): 0,
(43.2% identity in 389 aa overlap); etc. Contains P800017
ATP/GTP-binding site motif A (P-loop) and P801008 DnaA
protein signature. BELONGS TO THE DnaA FAMILY. Note that
the first base of this gene has been taken as base 1 of
the Mycobacterium bovis genomic sequence."
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(99.8% identity in 402 aa overlap). dnaA, DNA polymerase
III (beta chain) (EC 2.7.7.7) (see citations below).
equivalent to other Mycobacterial DNA POLYMERASES III BETA
CHAIN e.g. NP_301130.1|NC_002677 from Mycobacterium leprae
(399 aa); Q9L7L6|DnaA_MYC from Mycobacterium avium
subsp. paratuberculosis (399 aa); P52851|DnaA_MYC from

Mycobacterium smegmatis (397 aa); etc. Also highly similar to others e.g. P27903|DP3B_STRCO DNA POLYMERASE III BETA CHAIN from Streptomyces coelicolor (376 aa), FASTA scores: opt: 1189, E(): 0, (52.8% identity in 337 aa overlap); P21174|DP3B_MICLU from Micrococcus luteus (310 aa); P52023|DP3B_SYN7 from Synecoccus sp. strain PCC 7942 (375 aa); etc. Overlaps and extends CDS in neighbouring cosmid MTCV10H4.01."

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LPMLTGIVELGETVLAATDFRLAVRELKWSASSPDIEAIVLPAKTLAEAKAG
IGGSVRLSLGTGPGVGDGLGTSNGKRSITRLLDAEPFKQLLPTEHTAVATWD
VAELTEALIKVALVADRAQVMEFADGVSRLSAGADVDGRAEEDLVVDYAGEPLTIA
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CDS

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IGGSVRLSLGTGPGVGDGLGTSNGKRSITRLLDAEPFKQLLPTEHTAVATWD
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(99.5% identity in 385 aa overlap). recF, DNA replication
and repair protein (see citations below), equivalent to
others Mycobacterial DNA replication and repair proteins
e.g. NP_301131.1|NC_002677 from Mycobacterium leprae (385
aa); Q9L7L5|REC_F MYCPA from Mycobacterium avium subsp.
paratuberculosis (385 aa); P50916|REC_F MYCSM from
Mycobacterium smegmatis (384 aa); etc. Also highly similar
to others e.g. P36176|REC_F STRCO DNA REPLICATION AND
REPAIR PROTEIN from Streptomyces coelicolor (373 aa);
NP_440892.1|NC_000911 from Synecocystis sp. strain PCC
6803 (384 aa); NP_469352.1|NC_003212 from Listeria innocua
(370 aa); etc. Contains P50017 ATP/GTP-binding site motif
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187 aa, from Mycobacterium tuberculosis strain H37Rv,
(99.5% identity in 187 aa overlap). Conserved hypothetical
protein (see citation below) highly similar, but longer
21 aa in N-terminus, to AAF33696.1|AF222789 unknown
protein from Mycobacterium avium subsp. paratuberculosis
(166 aa); and highly similar to NP_301132.1|NC_002677
conserved hypothetical protein from Mycobacterium leprae
(189 aa); S70990 hypothetical protein from Mycobacterium
smegmatis (194 aa). Also similar to in C-terminus to

C-terminal part of P35925|YREG_STRCO HYPOTHETICAL 19.8 KDA
PROTEIN (IN REC_F-GYR_B INTERGENIC REGION) from Streptomyces
coelicolor (190 aa), FASTA scores: opt: 404, E(): 3.9e-18,
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subunit B (EC 5.99.1.3) (see citations below), equivalent,
except in N-terminus, to other Mycobacterial DNA GYRASES
SUBUNIT B e.g. T10005 from Mycobacterium leprae (697 aa);
Q9L7L3|GYR_B MYCPA from Mycobacterium avium subsp.
paratuberculosis (677 aa) (has its N-terminus shorter);
P48355|GYR_B MYCSM from Mycobacterium smegmatis (675 aa);
etc. Also highly similar to others e.g. T10969 from
Streptomyces coelicolor (686 aa); P50075|GYR_B STSRH from

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Best Local Similarity 100.0%; Pred. No. 1.4e-57; Indels 0; Gaps 0;
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RESULT 13

AR169152

LOCUS

DEFINITION

AR169152

ACCESSION

AR169152.1

VERSION

GI:17906927

KEYWORDS

SOURCE

447 bp DNA linear PAT 17-DEC-2001

Sequence 4 from patent US 6290969.

ORGANISM Unknown.
 UNCLASSIFIED
 1 (bases 1 to 447)
 REFERENCE Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 AUTHORS Vedvick, T.S. and Twardzik, D.R.
 TITLE Compounds and methods for immunotherapy and diagnosis of
 tuberculosis
 JOURNAL Patent: US 6290969-A 4 18-SEP-2001;
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ORIGIN

Query Match 99.6%; Score 394.4; DB 6; Length 447;
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 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED
 1 (bases 1 to 447)
 REFERENCE Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 AUTHORS Vedvick, T.S. and Twardzik, D.R.
 TITLE Compounds and methods for diagnosis of tuberculosis
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ORIGIN

Query Match 99.6%; Score 394.4; DB 6; Length 447;
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Db	131	ATCGGGCCCTACCGCTTCTCGCTTGGGTGTTCGACAAACAAACGGCAACGGCGCACGA	190			
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Db	371	ACAGGGAACGTGACATTCGCGGAGGACCGGCGCCCGCC	406			
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LOCUS	AR194825	447 bp	DNA linear PAT 20-APR-2002			
DEFINITION	Sequence 4 from patent US 6350456.					
ACCESSION	AR194825					
VERSION	AR194825.1 GI:20244262					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 447)					
AUTHORS	Reed,S.G., Skeiky,Y.A.W. and Dillon,D.C.					
TITLE	Compositions and methods for the prevention and treatment of M. tuberculosis infection					
JOURNAL	Patent: US 6350456-A 4 26-FEB-2002;					
FEATURES	Location/Qualifiers					
source	1..447					
/organism="unknown"						
/mol_type="unassigned DNA"						
ORIGIN						
Query Match	99.6%;	Score 394.4;	DB 6; Length 447;			
Best Local Similarity	99.7%;	Pred. No. 9e-57;	1; Indels 0; Gaps 0;			
Matches	395;	Conservative 0;	Mismatches 1;			
Qy	1	ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGTGGCGAGGATTCGCCATTCGATC	60			
Db	11	ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGTGGCGAGGATTCGCCATTCGATC	70			
Qy	61	GGGCGAGCGATGGCGATTCGGGCGGACGATCCGATCGGTGGGGGTCAACCGCGTTCAT	120			
Db	71	GGGCGAGCGATGGCGATTCGGGCGGACGATCCGATCGGTGGGGGTCAACCGCGTTCAT	130			
Qy	121	ATCGGGCCTACCGCTTCTCGCTTGGGTGTTCGACAAACAAACGGCAACGGCGCACGA	180			
Db	131	ATCGGGCCTACCGCTTCTCGCTTGGGTGTTCGACAAACAAACGGCAACGGCGCACGA	190			
Qy	181	GTCCAAACGGTGTTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG	240			
Db	191	GTCCAAACGGTGTTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG	250			
Qy	241	ATCACCGCGGTGACGGCGCTCGGATCACTGGGCGCACCGCGATGGCGGACCGGCTTAAC	300			
Db	251	ATCACCGCGGTGACGGCGCTCGGATCACTGGGCGCACCGCGATGGCGGACCGGCTTAAC	310			

QY 301 GGGCATATCCGGTACGTCATCTCGTGACCTGGCAACCAAGTCGGGGGACGCGT 360
 Db 311 GGGCATATCCGGTACGTCATCTCGTGACCTGGCAACCAAGTCGGGGGACGCGT 370
 QY 361 ACAGGAACGTGACATTCGGCCAGGAGCCCGCGCC 396
 Db 371 ACAGGAACGTGACATTCGGCCAGGAGCCCGCGCC 406

RESULT 16
 AR233097
 LOCUS AR233097 447 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 4 from patent US 6458366.
 ACCESSION AR233097
 VERSION AR233097.1 GI:27275533
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 447)
 AUTHORS Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
 TITLE Compounds and methods for diagnosis of tuberculosis
 JOURNAL Patent: US 6458366-A 4 01-OCT-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 99.6%; Score 394.4; DB 6; Length 447;
 Best Local Similarity 99.7%; Pred. No. 9e-57;
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACGGCGCGTCCGATAACTTCCAGTGTCCAGGTGGGAGGATTCGCCATTCCGATC 60
 Db 11 ACGGCGCGTCCGATAACTTCCAGTGTCCAGGTGGGAGGATTCGCCATTCCGATC 70
 QY 61 GGGCAGGCGATGGGATTCGCGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCA 120
 Db 71 GGGCAGGCGATGGGATTCGCGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCA 130
 QY 121 ATCGGCGCTACCGCTTCTCGGCTTGGTGTGTCGACAAACGCGCAACGGGCGCAGA 180
 Db 131 ATCGGCGCTACCGCTTCTCGGCTTGGTGTGTCGACAAACGCGCAACGGGCGCAGA 190
 QY 181 GTCCAAACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
 Db 191 GTCCAAACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 250
 QY 241 ATCAGCGCGGTGACGGCGCTCGATCACTCGGCGCAGCGATGGCGGACGCGTTAAC 300
 Db 251 ATCAGCGCGGTGACGGCGCTCGATCACTCGGCGCAGCGATGGCGGACGCGTTAAC 310
 QY 301 GGGCATATCCGGTACGTCATCTCGTGACCTGGCAACCAAGTCGGGGGACGCGT 360
 Db 311 GGGCATATCCGGTACGTCATCTCGTGAACTGGCAACCAAGTCGGGGGACGCGT 370

RESULT 17
 AR353302
 LOCUS AR353302 447 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 4 from patent US 6592877.
 ACCESSION AR353302
 VERSION AR353302.1 GI:33759108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 447)
 AUTHORS Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,
 Vedvick, T.S., and Twardzik, D.R.
 TITLE Compounds and methods for immunotherapy and diagnosis of tuberculosis
 JOURNAL Patent: EP 1203817-A 4 08-MAY-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 99.6%; Score 394.4; DB 6; Length 447;
 Best Local Similarity 99.7%; Pred. No. 9e-57;
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 447)
 AUTHORS Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
 TITLE Compounds and methods for immunotherapy and diagnosis of tuberculosis
 JOURNAL Patent: US 6592877-A 4 15-JUL-2003;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 99.6%; Score 394.4; DB 6; Length 447;
 Best Local Similarity 99.7%; Pred. No. 9e-57;
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACGGCGCGTCCGATAACTTCCAGTGTCCAGGTGGGAGGATTCGCCATTCCGATC 60
 Db 11 ACGGCGCGTCCGATAACTTCCAGTGTCCAGGTGGGAGGATTCGCCATTCCGATC 70
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 Db 71 GGGCAGGCGATGGGATTCGCGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCA 130
 QY 121 ATCGGCGCTACCGCTTCTCGGCTTGGTGTGTCGACAAACGCGCAACGGGCGCAGA 180
 Db 131 ATCGGCGCTACCGCTTCTCGGCTTGGTGTGTCGACAAACGCGCAACGGGCGCAGA 190
 QY 181 GTCCAAACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
 Db 191 GTCCAAACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 250
 QY 241 ATCAGCGCGGTGACGGCGCTCGATCACTCGGCGCAGCGATGGCGGACGCGTTAAC 300
 Db 251 ATCAGCGCGGTGACGGCGCTCGATCACTCGGCGCAGCGATGGCGGACGCGTTAAC 310
 QY 301 GGGCATATCCGGTACGTCATCTCGTGACCTGGCAACCAAGTCGGGGGACGCGT 360
 Db 311 GGGCATATCCGGTACGTCATCTCGTGAACTGGCAACCAAGTCGGGGGACGCGT 370

RESULT 18
 AX429596
 LOCUS AX429596 447 bp DNA linear PAT 21-JUN-2002
 DEFINITION Sequence 4 from Patent EP1203817.
 ACCESSION AX429596
 VERSION AX429596.1 GI:21540845
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 AUTHORS Read, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,
 Vedvick, T.S., and Twardzik, D.R.
 TITLE Compounds and methods for immunotherapy and diagnosis of tuberculosis
 JOURNAL Patent: EP 1203817-A 4 08-MAY-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unidentified"
 /mol_type="unassigned DNA"
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ORIGIN
 Query Match 99.6%; Score 394.4; DB 6; Length 447;
 Best Local Similarity 99.7%; Pred. No. 9e-57;
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCTGGGAGGGATTCCGCAATCCGATC 60
Db 11 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCTGGGAGGGATTCCGCAATCCGATC 70
QY 61 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTAT 120
Db 71 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTAT 130
QY 121 ATCGGGCTACCGCTTCCCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGGCGACGA 180
Db 131 ATCGGGCTACCGCTTCCCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGGCGACGA 190
QY 181 GTCCAGCGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 240
Db 191 GTCCAGCGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 250
QY 241 ATCACCGCGTTCGACGCGCTCCGATCAACTCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 300
Db 251 ATCACCGCGTTCGACGCGCTCCGATCAACTCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 310
QY 301 GGGCATCATCCGCTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 396
Db 371 ACAGGAACTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 406
RESULT 20
BD006325 447 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PF 07-OCT-1997 JP 1998518432
PR 11-OCT-1996 US 08/729622.13-MAR-1997 US 08/818111 PI
STEVEN G REED,YASIR A W SKEIKY,DILLON D C,Neto,A.C., Houghton,R.,
NETO,
PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31,C07K14/35,C07K16/12,C12Q1/68,C12N15/62,G01N33/53 CC
Strandedness: Single;
CC Topology: Linear;
FH Key 1. 447 Location/Qualifiers
FT source /organism='Unidentified'.
FT Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

Db 251 ATCACCGCGTTCGACGCGCTCCGATCAACTCGGCGCAAGTGGGGCGGCGCGT 310
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Db 311 GGGCATCATCCGCTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 370
QY 361 ACAGGAACTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 396
Db 371 ACAGGAACTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 406
RESULT 20
BD006325 447 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PF 07-OCT-1997 JP 1998518432
PR 11-OCT-1996 US 08/729622.13-MAR-1997 US 08/818111 PI
STEVEN G REED,YASIR A W SKEIKY,DILLON D C,Neto,A.C., Houghton,R.,
NETO,
PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31,C07K14/35,C07K16/12,C12Q1/68,C12N15/62,G01N33/53 CC
Strandedness: Single;
CC Topology: Linear;
FH Key 1. 447 Location/Qualifiers
FT source /organism='Unidentified'.
FT Location/Qualifiers
1. 447
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

QY 1 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCTGGGAGGGATTCCGCAATCCGATC 60
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QY 61 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTAT 120
Db 71 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTAT 130
QY 121 ATCGGGCTACCGCTTCCCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGGCGACGA 180
Db 131 ATCGGGCTACCGCTTCCCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGGCGACGA 190
QY 181 GTCCAGCGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 240
Db 191 GTCCAGCGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 250
QY 241 ATCACCGCGTTCGACGCGCTCCGATCAACTCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 300
Db 251 ATCACCGCGTTCGACGCGCTCCGATCAACTCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 310
QY 301 GGGCATCATCCGCTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 396
Db 371 ACAGGAACTGACATTCGGCTGAACTGGCAAAACAAAGTGGGGCGGCGCGT 406
RESULT 19
AX832581
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match 99.6%; Score 394.4; DB 6; Length 447;
Best Local Similarity 99.7%; Pred. No. 9e-57;
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCTGGGAGGGATTCCGCAATCCGATC 60
Db 11 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCTGGGAGGGATTCCGCAATCCGATC 70
QY 61 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTAT 120
Db 71 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTAT 130
QY 121 ATCGGGCTACCGCTTCCCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGGCGACGA 180
Db 131 ATCGGGCTACCGCTTCCCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGGCGACGA 190
QY 181 GTCCAGCGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 240
Db 191 GTCCAGCGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 250
QY 241 ATCACCGCGTTCGACGCGCTCCGATCAACTCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 300

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QY 301 GGGCATATCCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGCGGCGACGCGT 360
Db 311 GGGCATATCCCGGTGACGTCACTCGGTGAACTGGCAACCAAGTCGGCGGCGACGCGT 370
QY 361 ACAGGGAACGTGACATTGGCGGAGGAGCCCGCGCC 396
Db 371 ACAGGGAACGTGACATTGGCGGAGGAGCCCGCGCC 406

RESULT 21
BD06445 447 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION
Compounds and methods for immunotherapy and diagnosis of
Tuberculosis.
ACCESSION
BD06445
VERSION
BD06445.1 GI:18634816
KEYWORDS
JP 2001501832-A/4.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.
Compounds and methods for immunotherapy and diagnosis of
Tuberculosis.
PATENT: JP 2001501832-A 4 13-FEB-2001;
CORIXA CORP
JOURNAL
OS Unidentified
COMMENT
PN JP 2001501832-A/4
PD 13-FEB-2001
PF 07-OCT-1997 JP 1998518456
PR 11-OCT-1996 US 08/730510, 13-MAR-1997 US 08/818112 PI
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31, C07K14/35, A61K39/04, A61K48/00, A61K49/00, C12N15/62,
PC G01N33/50, G01N33/60, G01N33/569, C12N1/19, C12N1/20, C12N1/21, PC
C12N5/10//
PC (C12N1/21, C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..447
/organism="Unidentified".
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 99.6%; Score 394.4; DB 6; Length 447;
Best Local Similarity 99.7%; Pred. No. 9e-57; Mismatches 1; Indels 0; Gaps 0;
Matches 395; Conservative 0;

QY 1 ACGGCCCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 60
Db 11 ACGGCCCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 70
QY 61 GGGCAGCGATGCGATCGGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCAT 120
Db 71 GGGCAGCGATGCGATCGGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCAT 130
QY 121 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTGTCACAAACGCGCAACGCGCGACGA 180
Db 131 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTGTCACAAACGCGCAACGCGCGACGA 190
QY 181 GTCCAAACGCGTGTGCGGAGCGCTCCGGCGGCGAAGTCTCGGATCTCCACCGGCGACGTG 240
Db 191 GTCCAAACGCGTGTGCGGAGCGCTCCGGCGGCGAAGTCTCGGATCTCCACCGGCGACGTG 250

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QY 241 ATCACCGCGTTCGACGCGCTCCGATCAATCTGGCCACCGCGATGGCGGACGCGCTTAAC 300
Db 251 ATCACCGCGTTCGACGCGCTCCGATCAATCTGGCCACCGCGATGGCGGACGCGCTTAAC 310
QY 301 GGGCATATCCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGCGGCGACGCGT 360
Db 311 GGGCATATCCCGGTGACGTCACTCGGTGAACTGGCAACCAAGTCGGCGGCGACGCGT 370
QY 361 ACAGGGAACGTGACATTGGCGGAGGAGCCCGCGCC 396
Db 371 ACAGGGAACGTGACATTGGCGGAGGAGCCCGCGCC 406

RESULT 22
BD069285 447 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION
Compounds and methods for immunotherapy and diagnosis of
Tuberculosis.
ACCESSION
BD069285
VERSION
BD069285.1 GI:22614888
KEYWORDS
JP 2001517069-A/4.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
Vedvick, T.H. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of
Tuberculosis.
PATENT: JP 2001517069-A 4 02-OCT-2001;
CORIXA CORP
JOURNAL
OS Unidentified
COMMENT
PN JP 2001517069-A/4
PD 02-OCT-2001
PF 30-AUG-1996 JP 1997511464
PR 01-SEP-1995 US 08/523436, 22-SEP-1995 US 08/533634 PR
22-MAR-1996 US 08/620874, 05-JUN-1996 US 08/659683 PR
12-JUL-1996 US 08/680574
PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC
C12N15/31, C07K14/35, A61K38/16, C12N15/62, G01N33/569, C12Q1/68, PC
C12N5/10.
PC C12N1/21//A61K39/04, (C12N1/21, C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..447
/organism="Unidentified".
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 99.6%; Score 394.4; DB 6; Length 447;
Best Local Similarity 99.7%; Pred. No. 9e-57; Mismatches 1; Indels 0; Gaps 0;
Matches 395; Conservative 0;

QY 1 ACGGCCCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 60
Db 11 ACGGCCCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 70
QY 61 GGGCAGCGATGCGATCGGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCAT 120
Db 71 GGGCAGCGATGCGATCGGGCGCAGATCCGATCGGTGGGGGTACCCACCGTTTCAT 130
QY 121 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTGTCACAAACGCGCAACGCGCGACGA 180
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QY 181 GTCCACCGGTGGTCCGGAGCGCTCCGGGCGCAAGTCTCGGCATCTCCACGGGCGAGTG 240
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 QY 241 ATCACCGCGGTGCAGCGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
 Db 251 ATCACCGCGGTGCAGCGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310
 QY 301 GGGCATCATCCGGTGCAGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
 Db 311 GGGCATCATCCGGTGCAGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 370
 QY 361 ACAGGAACGTCGACATTCGCGGAGGAGACCCCGGCC 396
 Db 371 ACAGGAACGTCGACATTCGCGGAGGAGACCCCGGCC 406

RESULT 23
 BD205817
 LOCUS 447 bp DNA linear PAT 17-JUL-2003
 DEFINITION Compounds and methods for diagnosis of tuberculosis.
 ACCESSION BD205817
 VERSION BD205817.1 GI:33015587
 KEYWORDS JP 2002530050-A/4.
 SOURCE Mycobacterium tuberculosis
 ORGANISM Mycobacterium tuberculosis
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 1 (bases 1 to 447)
 REED, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
 Vedwick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
 Compounds and methods for diagnosis of tuberculosis
 Patent: JP 2002530050-A 4 17-SEP-2002;
 CORIXA CORP
 OS Mycobacterium tuberculosis
 PN JP 2002530050-A/4
 PD 17-SEP-2002
 PF 17-FEB-1999 JP 2000532132
 PR 18-FEB-1998 US 09/024753, 05-MAY-1998 US 09/072596 PI
 STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI
 NETO, RAYMOND HOUGHTON, THOMAS S VEDWICK, DANIEL R TWARDZIK, MICHAEL J
 PI LODES,
 PI RONALD C HENDRICKSON
 PC C12N15/09, C07H21/02, C07K14/35, C07K16/12, PC
 C07K17/00,
 PC C07K19/00, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/04, C12Q1/
 68,
 PC G01N33/569, G01N33/68//A61K38/00, A61K39/04, A61K39/395, A61K39/
 395, A61P31/06
 PC (C12N1/21, C12R1/19), C12N15/00, C12N5/00, A61K37/02 CC
 Compounds and methods for diagnosis of tuberculosis. FH Key
 Location/Qualifiers
 FT source 1. .447
 FT Location/Qualifiers
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 /organism="Mycobacterium tuberculosis"
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ORIGIN
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 Best Local Similarity 99.7%; Pred. No. 9e-57;
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ACAGCGCGGTCCGATCACTTCAGGTGTCAGGGTGGCGAGGATTCGGCATTCGGATC 60
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 QY 61 GGGCAGCGGATCGGATCGCGGCGCAGATCCGATCGGTGGGGGTGACCCACCGCTTCAT 120

Db 71 GGGCAGCGGATCGGATCGCGGCGCAGATCCGATCGGTGGGGGTGACCCACCGTTTCAT 130
 QY 121 ATCGGGCGCTACCGGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGCGGACGA 180
 Db 131 ATCGGGCGCTACCGGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGCGGACGA 190
 QY 181 GTCCAAACCGGTGGTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAGTG 240
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 QY 241 ATCACCGCGGTGCAGCGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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 QY 301 GGGCATCATCCGGTGCAGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
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 QY 361 ACAGGAACGTCGACATTCGCGGAGGAGACCCCGGCC 396
 Db 371 ACAGGAACGTCGACATTCGCGGAGGAGACCCCGGCC 406

RESULT 24
 AR169165
 LOCUS 1872 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 17 from patent US 6290969.
 ACCESSION AR169165
 VERSION AR169165.1 GI:17906947
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1872)
 REED, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedwick, T.S. and Twardzik, D.R.
 Compounds and methods for immunotherapy and diagnosis of
 tuberculosis
 Patent: US 6290969-A 17 18-SEP-2001;
 Location/Qualifiers
 1. 1872
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 98.8%; Score 391.2; DB 6; Length 1872;
 Best Local Similarity 99.2%; Pred. No. 2.4e-56;
 Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ACAGCGCGGTCCGATCACTTCAGGTGTCAGGGTGGCGAGGATTCGGCATTCGGATC 60
 Db 758 ACAGCGCGGTCCGATCACTTCAGGTGTCAGGGTGGCGAGGATTCGGCATTCGGATC 817
 QY 61 GGGCAGCGGATCGGATCGCGGCGCAGATCCGATCGGTGGGGGTGACCCACCGTTTCAT 120
 Db 818 GGGCAGCGGATCGGATCGCGGCGCAGATCCGATCGGTGGGGGTGACCCACCGTTTCAT 877
 QY 121 ATCGGGCGCTACCGGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGCGGACGA 180
 Db 878 ATCGGGCGCTACCGGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGCAACGCGGACGA 937
 QY 181 GTCCAAACCGGTGGTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAGTG 240
 Db 938 GTCCAAACCGGTGGTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGAGTG 997
 QY 241 ATCACCGCGGTGCAGCGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
 Db 998 ATCACCGCGGTGCAGCGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1057
 QY 301 GGGCATCATCCGGTGCAGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 360
 Db 1058 GGGCATCATCCGGTGCAGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 1117

QY 361 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 396
 Db 1118 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 1153

RESULT 25

AR192455
 LOCUS AR192455 1872 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 17 from patent US 633852.
 ACCESSION AR192455
 VERSION AR192455.1 GI:20225662
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES 1 (bases 1 to 1872)
 AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedvick, T.S., and Twardzik, D.R.
 TITLE Compounds and methods for diagnosis of tuberculosis
 JOURNAL Patent: US 633852-A 17 15-JAN-2002;
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 source Location/Qualifiers
 1..1872
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 /mol_type="unassigned DNA"

ORIGIN

Query Match 98.8%; Score 391.2; DB 6; Length 1872;
 Best Local Similarity 99.2%; Pred. No. 2.4e-56;
 Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 60
 Db 758 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 817
 QY 61 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 120
 Db 818 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 877
 QY 121 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 180
 Db 878 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 937
 QY 181 GTCCAAACGTCGCGGAGGACCCCGGCC 240
 Db 938 GTCCAAACGTCGCGGAGGACCCCGGCC 997
 QY 241 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 300
 Db 998 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 1057
 QY 301 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 360
 Db 1058 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 1117
 QY 361 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 396
 Db 1118 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 1153

RESULT 26

AR194838
 LOCUS AR194838 1872 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 17 from patent US 6350456.
 ACCESSION AR194838
 VERSION AR194838.1 GI:20244275
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES 1 (bases 1 to 1872)
 AUTHORS Reed, S.G., Skeiky, Y.A.W., and Dillon, D.C.
 TITLE Compounds and methods for the prevention and treatment of M. tuberculosis infection

JOURNAL Patent: US 6350456-A 17 26-FEB-2002;
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 source Location/Qualifiers
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ORIGIN

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 Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Db 758 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 817
 QY 61 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 120
 Db 818 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 877
 QY 121 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 180
 Db 878 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 937
 QY 181 GTCCAAACGTCGCGGAGGACCCCGGCC 240
 Db 938 GTCCAAACGTCGCGGAGGACCCCGGCC 997
 QY 241 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 300
 Db 998 ATCCGCGGTCGACGCGGTCGCGGAGGACCCCGGCC 1057
 QY 301 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 360
 Db 1058 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 1117
 QY 361 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 396
 Db 1118 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 1153

RESULT 27

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 LOCUS AR233110 1872 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 17 from patent US 6458366.
 ACCESSION AR233110
 VERSION AR233110.1 GI:27275546
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES 1 (bases 1 to 1872)
 AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
 TITLE Compounds and methods for diagnosis of tuberculosis
 JOURNAL Patent: US 6458366-A 17 01-OCT-2002;
 FEATURES
 source Location/Qualifiers
 1..1872
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 98.8%; Score 391.2; DB 6; Length 1872;
 Best Local Similarity 99.2%; Pred. No. 2.4e-56;
 Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 60
 Db 758 ACAGGACGTCGATTCGCGGAGGACCCCGGCC 817
 QY 61 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 120
 Db 818 GGGCAGGCGATGCGATTCGCGGAGGACCCCGGCC 877

QY 121 ATCGGCGCTACCGCTTCTCCGCTTGGGTGTTGTCGACAAACACGGCAACGGCGACGA 180
Db 878 ATCGGCGCTACCGCTTCTCCGCTTGGGTGTTGTCGACAAACACGGCAACGGCGACGA 937
QY 181 GTCCAAACGGCTGTCGGGAGCGCTCCGGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
Db 938 GTCCAAACGGCTGTCGGGAGCGCTCCGGGCAAGTCTCGGCATCTCCACCGGCGACGTG 997
QY 241 ATCACCGCGTTCGACGGCGCTCCGATCAACTCGGCCACCGCATGGCGGACCGCTTAAAC 300
Db 998 ATCACCGCGTTCGACGGCGCTCCGATCAACTCGGCCACCGCATGGCGGACCGCTTAAAC 1057
QY 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACGGT 360
Db 1058 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACGGT 1117
QY 361 ACAGGGAACGTGACATTTGGCCGAGGACCCCGGCC 396
Db 1118 ACAGGGAACGTGACATTTGGCCGAGGACCCCGGCC 1153
RESULT 29
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LOCUS AR353315 1872 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 17 from patent US 6592877.
ACCESSION AR353315
VERSION AR353315.1 GI:33759121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1872)
AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
TITLE Compounds and methods for immunotherapy and diagnosis of
tuberculosis
JOURNAL Patent: US 6592877-A 17 15-JUL-2003;
FEATURES Location/Qualifiers
source 1..1872
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 98.8%; Score 391.2; DB 6; Length 1872;
Best Local Similarity 99.2%; Pred. No. 2.4e-56;
Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACAGGCGCGTCCGATCACTTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGGATC 60
Db 758 ACAGGCGCGTCCGATCACTTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGGATC 817
QY 61 GGGCAGGCGATGGCGATCGGGCGCAGATCCGATCGGGTGGGGGTCAACCCACGGTTTCAAT 120
Db 818 GGGCAGGCGATGGCGATCGGGCGCAGATCCGATCGGGTGGGGGTCAACCCACGGTTTCAAT 877
QY 121 ATCGGCGCTACCGCTTCTCCGCTTGGGTGTTGTCGACAAACACGGCAACGGCGACGA 180
Db 878 ATCGGCGCTACCGCTTCTCCGCTTGGGTGTTGTCGACAAACACGGCAACGGCGACGA 937
QY 181 GTCCAAACGGCTGTCGGGAGCGCTCCGGGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
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Db 998 ATCACCGCGTTCGACGGCGCTCCGATCAACTCGGCCACCGCATGGCGGACCGCTTAAAC 1057
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QY 361 ACAGGGAACGTGACATTTGGCCGAGGACCCCGGCC 396
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RESULT 29
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LOCUS AR353315 1872 bp DNA linear PAT 12-DEC-2003
DEFINITION Sequence 17 from Patent EP1347055.
ACCESSION AR353315
VERSION AR353315.1 GI:39840644
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
Vedvick, T.S., Twardzik, D.R. and Dillon, D.C.

Db 1118 ACAGGGAACGTGACATTTGGCCGAGGACCCCGGCC 1153
RESULT 29
AX429609
LOCUS AX429609 1872 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 17 from Patent EP1203817.
ACCESSION AX429609
VERSION AX429609.1 GI:21540858
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,
Vedvick, T.S. and Twardzik, D.R.
TITLE Compounds and methods for immunotherapy and diagnosis of
tuberculosis
JOURNAL Patent: EP 1203817-A 17 08-MAY-2002;
FEATURES Location/Qualifiers
source 1..1872
/organism="unidentified"
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ORIGIN
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Best Local Similarity 99.2%; Pred. No. 2.4e-56;
Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACAGGCGCGTCCGATCACTTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGGATC 60
Db 758 ACAGGCGCGTCCGATCACTTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGGATC 817
QY 61 GGGCAGGCGATGGCGATCGGGCGCAGATCCGATCGGGTGGGGGTCAACCCACGGTTTCAAT 120
Db 818 GGGCAGGCGATGGCGATCGGGCGCAGATCCGATCGGGTGGGGGTCAACCCACGGTTTCAAT 877
QY 121 ATCGGCGCTACCGCTTCTCCGCTTGGGTGTTGTCGACAAACACGGCAACGGCGACGA 180
Db 878 ATCGGCGCTACCGCTTCTCCGCTTGGGTGTTGTCGACAAACACGGCAACGGCGACGA 937
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QY 241 ATCACCGCGTTCGACGGCGCTCCGATCAACTCGGCCACCGCATGGCGGACCGCTTAAAC 300
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QY 301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACGGT 360
Db 1058 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACGGT 1117
QY 361 ACAGGGAACGTGACATTTGGCCGAGGACCCCGGCC 396
Db 1118 ACAGGGAACGTGACATTTGGCCGAGGACCCCGGCC 1153
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AX832594
LOCUS AX832594 1872 bp DNA linear PAT 12-DEC-2003
DEFINITION Sequence 17 from Patent EP1347055.
ACCESSION AX832594
VERSION AX832594.1 GI:39840644
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
Vedvick, T.S., Twardzik, D.R. and Dillon, D.C.

TITLE Compounds for immunotherapy and diagnosis of tuberculosis
JOURNAL Patent: EP 1347055-A 17 24-SEP-2003;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..1872
/organism="unidentified"
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ORIGIN

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Best Local Similarity 99.2%; Pred. No. 2.4e-56;
Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 61 GGGCAGCGGATGGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCACCCACCGTTTCA 120
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Qy 878 ATCGGGCTACGGCTTCCTCGGCTTGGGTGTTGTCACACACGCGACGGCGCACGA 937
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Qy 181 GTCCAAACGCGTGGTCCGGAGCGCTCCGGCGGCAAGTCTTCGGCATCTCCACCGCGACGTG 240
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Qy 361 ACAGGGAACGTGACATTTGGCGAGGAGCCCCCGGCC 396
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Job time : 6636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 04:41:08 ; Search time 2046 Seconds
(without alignments)
5779.777 Million cell updates/sec

Title: US-09-684-215B-3
Perfect score: 396
Sequence: 1 acggccgctccgataactt.....tggccgaggagcccccgcc 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

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7: em_estro:*

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11: gb_est3:*

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13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

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22: em_gss_mam:*

23: em_gss_mus:*

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27: em_gss_vrl:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	55.6	14.0	603	A2934428	A2934428 BJ_Ba000
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5	49.2	12.4	561	28	BH020987
6	48.6	12.3	634	10	BE361689
7	47.8	12.1	831	28	CC334434
8	47.6	12.0	289	29	P864L
9	47.4	12.0	731	13	EX626840
10	47.4	12.0	935	29	CNS006XK
11	47	11.9	1009	29	CNS010EW
12	46.4	11.7	515	13	EX424977
13	45.8	11.6	472	14	CB620050
14	45.6	11.5	515	13	EX424977
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17	45.4	11.5	582	29	CG234774
18	45.4	11.5	707	29	CC678226
19	45.4	11.5	777	29	CG326745
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31	44.4	11.2	632	28	BH189865
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34	44	11.1	419	14	CF432426
35	44	11.1	428	14	CF485159
36	44	11.1	458	14	CF486070
37	44	11.1	493	10	BE355002
38	44	11.1	536	12	BG412839
39	44	11.1	555	14	CF484008
40	44	11.1	575	14	CD222185
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ALIGNMENTS

RESULT 1

U82114

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

FURNED

COMMENT

U82114 289 bp DNA linear GSS 16-FEB-2001
U82114 ordered cosmid library Mycobacterium leprae genomic clone
cosmid L-373; contig 64, genomic survey sequence.

U82114.1 GI:3647212

GSS.

Mycobacterium leprae

Mycobacterium leprae

Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

1 (bases 1 to 289)

Silbaq, F.S., Cho, S.N., Cole, S.T. and Brennan, P.J.

Characterization of a 34-kilodalton protein of Mycobacterium leprae

that is isologous to the immunodominant 34-kilodalton antigen of

Mycobacterium paratuberculosis

Infect. Immun. 66 (11), 5576-5579 (1998)

99003183

9784577

Contact: Silbaq FS

Microbiology

Colorado State University

Fort Collins, CO 80523, USA

Eiglmeyer, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Use

of an ordered cosmid library to deduce the genomic organization of

Mycobacterium leprae. Mol. Microbiol. 7 (2), 197-206 (1993)

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Class: unknown.
Location/Qualifiers
1..289
/organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db_xref="taxon:1769"
/clone="cosmid L-373; contig 64"
/clone_lib="ordered cosmid library"

ORIGIN
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Best Local Similarity 55.2%; Pred. No. 0.0046;
Matches 127; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

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QY 216 TCTGGCATCTCCACCGGACGATGATCACCAGCGGTGACGCGCTCCGATCACTCGGC 275
DB 93 TGGCGCGTTCCTCAAGGGGTGCTTCTCACTAAGTTCGACGACCGCTGATGATGCGC 152
QY 276 CACCGCGATGGCGGACGCGCTTAAGGCGATCATCCGGTGCATCTCGGTGACTG 335
DB 153 CGACGCGTGTGCTGCGTCCGCGTCCAGGCGACCGCGGTGACAAAGTGTGCTGACCTA 212
QY 336 GCACACCAAGTCGGCGCGCACGCGTACAGGGAACGTGACATTGGCCGAGG 385
DB 213 TCAGATCAGTCTGTAGCAGTCGACAGGTTTCAGGTACATCTCGGCAAG 262

RESULT 2
LOCUS BJ_Ba002108r B. japonicum BAC library Bradyrhizobium japonicum
DEFINITION genomic, genomic survey sequence.
ACCESSION AZ934428
VERSION AZ934428.1 GI:13776488
KEYWORDS GSS.
SOURCE Bradyrhizobium japonicum
ORGANISM Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE 1 (bases 1 to 603)
AUTHORS Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,
Goicoechea,J.I., Stacey,G., Sadowsky,M.J. and Wing,R.A.
TITLE A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
Genome
JOURNAL Genome Res. 11 (8), 1434-1440 (2001)
MEDLINE 21376150
PUBMED 11483585
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 553.
FEATURES
Location/Qualifiers
1..603
/organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
/strain="USDAL10"
/db_xref="taxon:375"
/lab_host="E. coli"
/clone_lib="B. japonicum BAC library"
/notes="Vector: pIndigo56; Site 1: HindIII"

ORIGIN
Query Match 14.0%; Score 55.6; DB 28; Length 603;
Best Local Similarity 54.4%; Pred. No. 0.42;

Matches 112; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 140 TCGGCTTGGGTGTGTGTCACAAACGCGACGCGGACAGTCCACGCGTGTTCGGGA 199
DB 363 TCGCGACAGCGCTCGGCATGAAGAAGCGCGGAGCGCGCTGTGGCGAGCGGCGGA 422
QY 200 GGGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGAGCGTGCATCACCGCGCTCGACGCGC 259
DB 423 ACGTCCGGCGGCGAAGCGCGCATCGAGTCGGCGAGTGCATCACCTCGTCAACGGCG 482
QY 260 CTCGATCAACTCGGCCACCGCGATGGCGGACGGCTTAACGGGCATCATCCGGTGAAG 319
DB 483 AATCGGTCAAGACGCCCGCGAGTTCGCCCGCACCATCGGCGCATGGCGGCCGCGTGCGA 542
QY 320 TCATCTCGGTGACCTGGCGCAACCAAG 345
DB 543 TCGTGAAGCTTAACGTGTGCACAAG 568

RESULT 3
LOCUS CNS0091P 925 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL053013
VERSION AL053013.1 GI:4934461
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilla.
REFERENCE 1 (bases 1 to 925)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE [E-mail : seqrefgenoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosier in Pister de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..925
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
/notes="end : TET3"

ORIGIN
Query Match 12.7%; Score 50.4; DB 29; Length 925;
Best Local Similarity 15.4%; Pred. No. 4.8;
Matches 53; Conservative 158; Mismatches 133; Indels 1; Gaps 1;

QY 53 TTCGATCGGCGAGCGATGGCGATCGGGGCGAGTCCGATCGGTGGGGGTCAACCA 112
DB 553 TTSSGGYGRKSGSGBSCSCSCSCSCSCSCSCSCSCSCSCSCSCSCSCSCSCS 612
QY 113 CCGTTCATATCGGCGCTTACCGCCTTCTCGCTTGGTGTTCGACAAACAGCGCAAG 172
```


QY 159 CAACACGGGCAACGGGCGACGAGTCCAAACGGGTGGTGGGAGCGCTCCGGGGGCAAGTCT 218
 Db 13 CGAGATCGGATCCCGCGCGCGCTGGTAGTCGAGGCGCGTGGGTCCCGCGGCTCGCT 72
 QY 219 CGGATCTCCACCGCGGCGGAGTATCACCGCGGTGGAGGGGCTCCGATCAACTCGGCC 276
 Db 73 CGGCATTCAACCGCGGCGGAGTATCTTGGCTTCAACGGCAACCGGATCAAGTCAGTC 130

RESULT 6
 BE361689/c
 LOCUS
 DEFINITION DGI_81_E06.g1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
 ACCESSION BE361689
 VERSION BE361689.1 GI:3303246
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 634)
 Cordonnier-Pratt,M.-X., Gingle,A., Marsala,C., Sudman,M. and
 Pratt,L.H.

TITLE An EST database from Sorghum: dark-grown seedlings
 JOURNAL Unpublished (2000)
 COMMENT Contact: Cordonnier-pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: PolyTMix
 High quality sequence start: 67
 High quality sequence stop: 634
 POLYA=No.

FEATURES
 source
 1..634
 Location/Qualifiers
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /db_xref="taxon:4558"
 /clone_lib="Dark Grown 1 (DGI)"
 /note="Organ: 5-day-old dark-grown seedlings; Vector:
 Lambda Zap; Site 1: XhoI; Site 2: EcoRI; The library was
 made from poly-A RNA in the cloning vector lambda ZAP II.
 Clones to be sequenced were prepared by mass excision."

ORIGIN
 Query Match 12.3%; Score 48.6; DB 10; Length 634;
 Best Local Similarity 47.0%; Pred. No. 10;
 Matches 150; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
 QY 17 ACTTCAGTGTCCAGGTTGGGCGGAGGATTCGCCATTCCGATCGGCGAGGCGATGGCGA 76
 Db 388 AGCAGTGTCCGTCACAGTAGTGGCAGCGCTTGTGGCCCGCAGCGCTGGCCCGTGGCGA 329
 QY 77 TCGCGGGCCAGATCCGATCGGTTGGGGGTCAACCCAGCTTCATATCGGGGCTACCGGCT 136
 Db 328 ACCCTTCGCGCAGATGTGTACCGGTGGGCGCCACCGGTAGAGTCTGCTCTCCCGACG 269
 QY 137 TCTCGGCTTGGTGTTCGACACACGCGACGCGACGAGTCCACGCGGTGTCG 196
 Db 268 AGACGTGTGTGTCGTGCTGCTCTCGAGTTCGGGCGCGGAAACGCTTCTGCTGCT 209
 QY 197 GGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGTTCGACG 256
 Db 208 GCGCGCGCGGCGGCGGCTACTGCTCCGGGCTGGCGGCTTGGCGGTGGAGCTTGT 149

QY 257 GCGTCCGATCAACTCGGCCACCGCATCGCGGCGGCTTAACGGGCATCATCCCGGTG 316
 Db 148 GCCCGCGGAGCCCTGGTACGACGCGAAGGCTTCCCGACACCGCGCACCGAACCGGA 89
 QY 317 ACCTCATCTCGGTGACCTG 335
 Db 88 GCTGCTCTCTCGTGGCCAG 70

RESULT 7
 CC334434/c
 LOCUS
 DEFINITION OGQ83TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0365N21,
 genomic survey sequence.

ACCESSION CC334434
 VERSION CC334434.1 GI:30803847
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 831)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Classes: sheared ends.

FEATURES
 source
 1..831
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMMBMA0365N21"
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 12.1%; Score 47.8; DB 28; Length 831;
 Best Local Similarity 57.1%; Pred. No. 15;
 Matches 109; Conservative 0; Mismatches 77; Indels 5; Gaps 1;
 QY 164 ACGGCAACGGCGCACGAGTCCACGGGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCA 223
 Db 777 ACGGCGACGGCGCGAGAGCGCGCTTCGTCGCCGCGACATCGCGG-----CTGCCCG 723
 QY 224 TCTCCACCGCGCGAGTGATCACCGCGTTCGACGGGCTCCGATCACTCGGCGCACCGCA 283
 Db 722 TCGCCACCTTCGACGTGCGCGGCTCGACGCGCGCCCGCGCTGACGCGCGCGCGCGCG 663
 QY 284 TGGCGACCGCTTAACGGGCATCATCCCGGTGACGTCTCTCGGTGACCTGCAACCA 343
 Db 662 GCGCTTCGCTCCGCGGCGGCGCTCTCCGCGACGCTCTCTCTCTCTCTCTCTCTCT 603
 QY 344 AGTCGGCGCGC 354
 Db 602 CCCCGCGCGC 592

RESULT 8
 P864L
 LOCUS
 DEFINITION Leishmania major Friedlin PAC P864 left end-sequence, genomic

QY 164 ACGGCAACGGCGCACGAGTCCACGGGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCA 223
 Db 777 ACGGCGACGGCGCGAGAGCGCGCTTCGTCGCCGCGACATCGCGG-----CTGCCCG 723
 QY 224 TCTCCACCGCGCGAGTGATCACCGCGTTCGACGGGCTCCGATCACTCGGCGCACCGCA 283
 Db 722 TCGCCACCTTCGACGTGCGCGGCTCGACGCGCGCCCGCGCTGACGCGCGCGCGCGCG 663
 QY 284 TGGCGACCGCTTAACGGGCATCATCCCGGTGACGTCTCTCGGTGACCTGCAACCA 343
 Db 662 GCGCTTCGCTCCGCGGCGGCGCTCTCCGCGACGCTCTCTCTCTCTCTCTCTCTCT 603
 QY 344 AGTCGGCGCGC 354
 Db 602 CCCCGCGCGC 592

RESULT 8
 P864L
 LOCUS
 DEFINITION Leishmania major Friedlin PAC P864 left end-sequence, genomic

survey sequence.
 AL390548
 VERSION AL390548.1 GI:9501524
 KEYWORDS GSS.
 SOURCE Leishmania major
 ORGANISM Leishmania major
 Leishmania major
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 1 (bases 1 to 289)
 Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.
 A physical map of the Leishmania major Friedlin genome
 Genome Res. 8 (2), 135-145 (1998)
 98146435
 9477341
 2 (bases 1 to 289)
 Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Barrell,R.G.
 Direct Submission
 Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk
 see http://www.ebi.ac.uk/parasites/leish.html
 Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/Lmajor/
 The primer sequence can be obtained from alicat@sanger.ac.uk.
 FEATURES
 source Location/Qualifiers
 1..289
 /organism="Leishmania major"
 /mol_type="genomic DNA"
 /strain="Friedlin"
 /db_xref="taxon:5664"
 /clone="PAC F864"
 ORIGIN
 Query Match 12.0%; Score 47.6; DB 29; Length 289;
 Best Local Similarity 62.7%; Pred. No. 13;
 Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 159 CAACAAGCGACGGGACGAGTCCACGGTGGTGGGAGCGCTCCGGCGCAAGTCT 218
 Db 24 CGAGAGCGGATCCCGCGCGCTGTAGTCGAGGGCGCTCGGGTCCCGGGTCCGCT 83
 QY 219 CGGATCTCCACCGCGGACGATGATCAGCGGCTCGAGCGGCTCCGATCAACTCGGC 276
 Db 84 CGGATTCACCGCGGACGATGATCCTGGCTTCAACGGCAGCGCGATCAAGTCAGTC 141
 RESULT 9
 BX626840
 LOCUS BX626840 NAPI Anopheles gambiae cDNA clone ANGPN122C12T7, mRNA
 DEFINITION
 ACCESSION BX626840.1 GI:33553685
 VERSION
 KEYWORDS
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
 1 (bases 1 to 731)
 Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.
 Anopheles gambiae EST, Center for Tropical Disease Research and Training
 Unpublished (2003)
 JOURNAL
 CONTACT: Frank H. Collins
 Center for Tropical Disease Research and Training
 University of Notre Dame
 Notre Dame, IN 46556, USA
 Tel: 574-631-9245
 Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

FEATURES
source

Location/Qualifiers
 1..731
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /db_xref="taxon:7165"
 /clone="ANGPN122C12T7"
 /lab_host="E. coli DH10B"
 /clone_lib="NAPI"
 /notes="Vector: pT73D-Pac (Pharmacia); Site 1: NotI; Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAPI is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 12.0%; Score 47.4; DB 13; Length 731;
 Best Local Similarity 51.2%; Pred. No. 18;
 Matches 111; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
 QY 156 CGACAACACGGCAACGGCGACAGTCCAAAGCGTGGTGGGAGCGTCCGGCGCAAG 215
 Db 49 CAACAACCAACAACAGTGCACCAAGTGCACCTCGTGGTGGGCGATCGAGCG 108
 QY 216 TCTGGCATCTCCACCGCGACGTGATCACCAGCGGTGACCGCGCTCCGATCAACTCGGC 275
 Db 109 GCTGTCTCAAGACGGGAGCGGTGCGCCCGTACGCCATCGGACGGCAACACGC 168
 QY 276 CACCGCATGGCGGACCGCTTAAACGGGCATCATCCCGGTGACGTCTCTCGGTGACTG 335
 Db 169 CACCGTATGGCGGCGCGACGCTCGGCCATCACACCGCATGAGCGCGGGAATCAC 228
 QY 336 GCAACCAAGTCGGGCGGACGCGGTACAGGGAAGCTG 372
 Db 229 GTACACCAACTGGACTACCCCGGTGTGTGAAGAG 265

RESULT 10

LOCUS

DEFINITION

CNS006XK 935 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence T7 end of BAC #
 BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 935)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammose in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

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1. Location/Qualifiers
  1. .1009
    /organism="Drosophila melanogaster"
    /mol_type="genomic DNA"
    /db_xref="taxon:7227"
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    /clone_lib="DrosBAC"
    /plasmid="pBe1cBAC11"
    /note="vnd : Sp6"

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/mol_type="genomic
/db_xref="taxon:722
/clone="BACN03P19"
/clone_lib="DrosBAC
/plasmId="pBelobAC1
/note="end : SP6"

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Best Local Similarity 30.8%; Pred: No. 23;
Matches 111; Conservative 80; Mismatches 168; Indels 1; Gaps 1;

[illegible]

ACCESSION
VERSION

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 515)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
 Genoscope, Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Division of

```

FEATURES
  source
    1. 515
      Location/Qualifiers
        /organism="Homo sapiens"
        /mol_type="mRNA"

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[illegible]

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 582)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG2BL96TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
source
1..582
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0753024"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSk-; Site:1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 11.5%; Score 45.4; DB 29; Length 582;
Best Local Similarity 57.5%; Pred. No. 42;
Matches 103; Conservative 0; Mismatches 71; Indels 5; Gaps 1;
Qy 164 ACGCACGGCGACGAGTCCACGGCTGTGGAGCGCTCGGGCGGCAAGTCTCGGCA 223
Db 280 ACGGGCACGGCGAGAGGCGGCTTCGTCTCGCGGAGCATCGGCGG-----CTGCCG 334
Qy 224 TCTCACGGCGACGTGATCACCGGCTGCACGGCGCTCCGATCAATCGGCCACCGCGA 283
Db 335 TCGCACCTTCGAGCTGGCGGCTCGACGCCGCCGCTGCACGGCGCGCGCGC 394
Qy 284 TGGCGGAGCGCTTAACGGGATCATCCGGTGACGTATCTCGGTGACTGCGCAACC 342
Db 395 GCGGCTTCGGTCGGGGGGCGGCTCTCCGCGACGTCCTCTCTCTCTCGCGTCC 453

RESULT 18
CC678226 707 bp DNA linear GSS 19-JUN-2003
OGWES86TV ZM_0.7 1.5 KB Zea mays genomic clone ZMMBma0561P03,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 707)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.

```

FEATURES
  source
    Location/Qualifiers
      1..707
        /organism="Zea mays"
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        /clone_lib="ZM 0.7 1.5 KB"
        /note="Vector: pCSK-; Site 1: HincII; 0.7-1.5 kb
        methylation filtered genomic DNA library"

ORIGIN
  Query Match      11.5%; Score 45.4; DB 29; Length 707;
  Best Local Similarity 57.5%; Pred. No. 44;
  Matches 103; Conservative 0; Mismatches 71; Indels 5; Gaps 1;

QY 164 AGGCACAGCGCCACAGATCCACCGCTGCTCGGAGCGCTCCGCGCGCAAGTCTCGCA 223
Db 11  ACGGCGACGGCGACAGAGCGCGCTTCGTCGTCGCGGACGATCGCGCG-----CTGCCG 65

QY 224 TCTCCACCGCGCAGCTGTATCACCGCGGTCGACGCGGCTCCGATCAATCGGCCACCGCA 283
Db 66  TCGCACCTTCGACGTGCGCGGCTCGACGCGCGCCCGCGCTGCACGCGCGCGCGCGC 125

QY 284 TGGCGACCGCGTTAACCGGCGATCATCCGCGTGACGTATCTCGGTGACCTGGCAAC 342
Db 126 GCGCTTCGCGTCCGCGCGCGCCCTCTCCGCGACGTCTCTCTCTCTCTCTCTCTCTCT 184

RESULT 19
CG326745/c
LOCUS
  DEFINITION
    genomic survey sequence.
  ACCESSION
    CG326745
  KEYWORDS
    CG326745.1 GI:34244011
  SOURCE
    Zea mays
    ORGANISM
      Zea mays
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
      clade; Panicoideae; Andropogoneae; Zea.
  REFERENCE
    1 (bases 1 to 777)
      Whitlaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
      Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
      Ctek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
      Consortium for Maize Genomics
      Unpublished (2002)
      Other GSSs: OG2AH31TH
      Contact: Cathy Whitlaw
  TIGR
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301-838-5843
    Fax: 301-838-0208
    Email: whitlaw@tigr.org
    Seq primer: TP
    Class: sheared ends.
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        1..777
          /organism="Zea mays"
          /mol_type="genomic DNA"
          /strain="B73"
          /db_xref="taxon:4577"
          /clone="ZMMBMA0742F14"
          /clone_lib="ZM 0.7 1.5 KB"
          /note="Vector: pCSK-; Site 1: HincII; 0.7-1.5 kb
          methylation filtered genomic DNA library"

ORIGIN
  Query Match      11.5%; Score 45.4; DB 29; Length 777;
  Best Local Similarity 57.5%; Pred. No. 45;
  Matches 103; Conservative 0; Mismatches 71; Indels 5; Gaps 1;

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GCOBH1TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMWBMA0344C06,
 genomic survey sequence.
 ACCESSION CC331586
 VERSION CC331586.1 GI:30800757
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 830)
 Whitelet,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.
 Location/Qualifiers
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 /clone_lib="ZM0.7_1.5_KB"
 /clone="ZMWBMA0344C06"
 /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
 ORIGIN
 Query Match 11.5%; Score 45.4; DB 28; Length 830;
 Best Local Similarity 57.5%; Pred.No.46;
 Matches 103; Conservative 0; Mismatches 71; Indels 5; Gaps 1;
 QY 164 ACGGCAACGGCGCACGAGTCCAAAGCGGTGTGCGGAGCGCTCGGGGGCAAGTCTCGGCA 223
 Db 389 ACGGGACGCGCGCAGAGGCGGTTCGTCTCGGCGCAGCATCGGCGG 335
 QY 224 TCTCCACGGCGGACGTATCACCGGCTGACGGCGTCCGATCACTCGGCCACCGCGA 283
 Db 334 TCGCCACCTTCGACGTGCGGCGCTGACGCCGCCGCCGCTGACGCCGCCGCCGCGC 275
 QY 284 TGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACC 342
 Db 274 GCGCTTCGCTCGCGGGCGCGCTCTCGGACGTCCTCTCTCTCTCGCGCTCC 216
 RESULT 22
 CK161968 1148 bp mRNA linear EST 05-DEC-2003
 LOCUS FGAS014551 Triticum aestivum FGAS: Library 4 Gate 8 Triticum
 DEFINITION aestivum cDNA, mRNA sequence.
 ACCESSION CK161968
 VERSION CK161968.1 GI:38990698
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.
 1 (bases 1 to 1148)
 Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
 Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
 Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,
 Penniket,C., Roach,J.L. and Sarnan,P.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)

COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgs_est@cs.usask.ca
This sequence is the direct result of the Base calling software
phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region 128-8311.
Plate: L48003 row: H column: 15.

FEATURES
source
1. 1148
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial
parts (crown and leaf) of wheat cultivars Norstar during
dehydration stress. 8 mRNA populations were combined
before constructing the library. The first four come from
removing plants from vermiculite (7 day old plants) and
incubating them at 20C on the bench without water for 1,
2, 3 and 4 days. The last four come from plants grown in
soil in a growth chamber after watering is terminated.
Four samplings were taken in a two week period; the first
after wilting was observed and the last, two weeks later,
consisted of live crown and stem tissue (leaf tissue was
yellow and dead). First strand synthesis in this library
was done in the presence of methylated dCTP thereby
protecting from internal cleavage with NotI."

ORIGIN
Query Match 11.5%; Score 45.4; DB 14; Length 1148;
Best Local Similarity 47.1%; Pred. No. 49;
Matches 139; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
Qy 64 CAGGCGATGGCGATCGCGGGCGAGATCGATCGGTGGGGGTCCACCCCGTTCATATC 123
Db 255 CTGGCCACGCTGATCGGGCGGAGCTCGCGGGGGGGCTCCGAGCGCGCGCTCGGC 314
Qy 124 GGGCTACCGCTTCTCGGCTTGGTGTTCGACACAAACGGGCGACGAGTC 183
Db 315 TACGCCACCGCGGTTCGCCAAGCGGGGAGGACTACTTCTTCGCAAGCTGACTGC 374
Qy 184 CAACGCGTGGTGGGAGCGCTCGCGCGCAAGTCTCGGCATCTCCACGGGCGAGTC 243
Db 375 CTCGCGTCCCGGCGACCCCTCCACCGCTTCTCGCTTCGCGGTTCGAGCGGCAC 434
Qy 244 ACCGCGTGGAGCGGCTTCGATCACTCGGCCACCGGATGGCGGAGCGGCTTAAAGG 303
Db 435 AACGGGTGTTCGGCGCGGTTCACGAAGGAGGACCTGTCTGGAGCACGTCATGAGCGC 494
Qy 304 CATCATCCGGTGGAGTATCTCGGTGACCTGGCAACCAAGTCGGGGCGACGC 358
Db 495 TCCCGCGCGACATCGGAGCGCGGAGGACTGGCTGCGAGGCTGCCCGCGCGC 549

RESULT 23
BE215641
LOCUS 538 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEB0007J02f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Blumeria challenged) Hordeum vulgare subsp. vulgare
cDNA clone HV_CEB0007J02f, mRNA sequence.
ACCESSION BE215641
VERSION BE215641.1 GI:8903169
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J.,
Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 199
Seq primer: AATTAACCTCTACTTAACGGG
High quality sequence stop: 462.

FEATURES
source
1. 538
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="C116151 (Mla6)"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HV_CEB0007J02f"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVCDNA0005 (Blumeria challenged)"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874
(avrMla6) of Blumeria graminis f. sp. hordei, and leaves
were harvested 20 and 24 hr post-inoculation and snap
frozen; uninoculated leaves were harvested 20 hr
post-inoculation (Wei, Wise). In the TJ Close lab at the
University of California, Riverside, total RNA was
prepared from each sample pool, equal quantities of all
three RNA pools were combined, poly(A) RNA was purified
from the mixture, one primary unamplified cDNA library was
made, and 1 million pfu were in vivo excised to give
phagescript SK(-) cDNA phagemids (Choi, Close). Phagemids
were plated and picked at the Clemson University Genomics
Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing).
Plasmid DNA preparations, DNA sequencing and sequence
analysis were performed at CUGI (Wing, Yu, Frisch, Henry,
Simmons, Oates, Rambo, Main). The sequence has been
trimmed to remove vector sequence and contains a minimum
of 100 bases of phred value 20 or above. For more details
on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders_Also
see clone TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gspages/bgn/31/cover.html")

ORIGIN
Query Match 11.4%; Score 45.2; DB 10; Length 538;
Best Local Similarity 48.6%; Pred. No. 45;
Matches 122; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
Qy 54 TCCGATCGGCGAGCGATCGGATCGGGCGGACGATCCGATCGGTGGGGGTCCACCCAC 113
Db 225 TGGCGTCCCGCTGGCCACGCTGATCGGGCGGAGCTCCGCGGGGGGTCCGAGGCGCC 284
Qy 114 CGTTTCATATCGGGCTACCGCCCTTCCTCGGCTTGGGTGTTCGACAAACACGCAACGG 173
Db 285 GCGCTCGGTACGGTCACCGCGCTTTCGAGCGGGGAGGACTACTTCTCTCTCAA 344

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1. (bases 1 to 538)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J.,
Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 199
Seq primer: AATTAACCTCTACTTAACGGG
High quality sequence stop: 462.

```

QY 174 GCGACGAGTCCACGCGGTGGTGGGAGCGCTCCGCGCGCAAGTCTCGGCATCTCCACCGG 233
Db 345 GCGCGACTGCTTCGCGTACCGCGCGACCCCTCCACCGCTTCTTCGTCTTCGCGGTGTT 404
QY 234 CGAGCTGATCACCGGCTCGACGGCTCCGATCACTCGGCCACCGGATGGCGGACGC 293
Db 405 CGACGGGCACACGGGGTGTGGGGCGGGGTTATCAGGAGGACCTGCTGGAGCAGT 464
QY 294 GCTTAACGGCG 304
Db 465 GATGAACGGCG 475

RESULT 24
LOCUS AUI91977
DEFINITION AUI91977 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis
          cDNA clone PF024a12_r 5', mRNA sequence.
ACCESSION AUI91977
VERSION AUI91977.1 GI:31930158
KEYWORDS EST.
SOURCE Porphyra yezoensis
ORGANISM Porphyra yezoensis
          Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
          Porphyra.
REFERENCE 1 (bases 1 to 502)
AUTHORS Asamizu,E., Nakajima,M., Kitade,Y., Saga,N., Nakamura,Y. and
          Tabata,S.
TITLE COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS
          OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TAG
          FREQUENCY ANALYSIS
JOURNAL J. Phycol. 39 (5), 923-930 (2003)
COMMENT Contact: Erika Asamizu
          The First Laboratory for Plant Gene Research
          Kazusa DNA Research Institute
          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
          Email: asamizu@kazusa.or.jp. URL:http://www.kazusa.or.jp/en/plant/.

FEATURES             source
     1..502
     /organism="Porphyra yezoensis"
     /mol_type="mRNA"
     /strain="TU-1"
     /db_xref="taxon:2788"
     /clone="PF024a12_r"
     /dev_stage="sporophytes"
     /clone_lib="porphyra yezoensis TU-1 sporophytes"

ORIGIN
Query Match      11.3%; Score 44.8; DB 9; Length 502;
Best Local Similarity 47.0%; Pred. No. 54;
Matches 139; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 57 GATCGGGCAGCGATGGCGATCGCGGCCAGATCCGATCGGTGGGGGTACCCACCGT 116
Db 74 GGTGGCGCGCGGTGGCGTTCAGGGGGTGGCCGACTGGGCAAGTCTCTGTACGCGC 133
QY 117 TCATATCGGGCTACCGCTTCTCGGTGGGTGTTGTCACACACGCAACGCGCGC 176
Db 134 AGGTGACTGGCTGCGCGCGGTGGTGGGACCGTTCACGGCGCCCGCTGGCGGGCGCGGTGC 193
QY 177 ACAGATCCAAACGCTGGTGGGAGCGCTCCGCGCGCAAGTCTCGGCATCTCCACCGCGA 236
Db 194 CGCGCGCTTCTGGCGTCAAGCGCCGACGCGGTCTGCCCGGTGGCGGTGGAGGGCAC 253
QY 237 CGTGATCACCGGTCAGCGCGCTCCGATCACTCGGCCACCGGATGGCGGACGCGCT 296
Db 254 CGCGGTGCCCGCGCGGTGTGGCGTCTCCCGCGGCACCCATGCGGTGGAGGTGT 313
QY 297 TAACGGGCATATCCCGGTGACGTATCTCGGTGACCTGGCAAAACCAAGTCCGGCG 352
Db 314 CTACGCCACCCCGCGCGGACGCGCGGTGTCTCGTGACCGCCCGCGCTGGTG 369

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RESULT 25
LOCUS CNS004NB
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
          BACR10E16 of RPCI-98 library from Drosophila melanogaster (fruit
          fly), genomic survey sequence.
ACCESSION AL054280
VERSION AL054280.1 GI:4931788
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 839)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
          collaboration with the Berkeley Drosophila Genome Project (BDGP).
          The BDGP is constructing a physical map of the Drosophila
          melanogaster genome using these BACs. For further information
          please see http://www.fruitfly.org The BDGP Drosophila
          melanogaster BAC library was prepared by Kazutoyo Osoegawa and
          Aaron Mammoler in Pieter de Jong's laboratory in the Department of
          Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
          NY. The library is named RPCI-98 and was constructed by partial
          EcoRI digestion of Drosophila DNA provided by the BDGP from the
          isogenic strain Y; cn bw sp, the same strain used for the BDGP's
          P1 and EST libraries. A more detailed description of the library
          and how to order individual BAC clones, the entire library, or
          filters for hybridization from the BACPAC Resource Center can be
          found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES             source
     1..839
     /organism="Drosophila melanogaster"
     /mol_type="genomic DNA"
     /db_xref="taxon:7227"
     /clone="BACR10E16"
     /clone_lib="RPCI-98"
     /note="end : TET3"

ORIGIN
Query Match      11.3%; Score 44.6; DB 29; Length 839;
Best Local Similarity 15.9%; Pred. No. 66;
Matches 59; Conservative 150; Mismatches 162; Indels 0; Gaps 0;

```

```

QY 5 CCGGTCCGATACTTCCAGCTGTCCAGGTGGCGGAGGATTCGCATTCGATCGGCG 64
Db 465 SMSSSACASASSSSGCSASSVAACSSACAGSAGSSSSSAGSSSAGSSGSG 524
QY 65 AGCGATGGCGATCGCGGCGCAGATCCGATCGGTGGGGGTCCACCCCGTTCATATCG 124
Db 525 ASGSRSGGAGSGGGGGGSRGSGCGGAVGASGSSSACSCSASSASSSSSAGCMSCS 584
QY 125 GGCTACCGCTTCTCTCGGCTGGGTGTGTCACAAACACGCAACGCGCACGATCC 184
Db 585 SSSSSSAAACSSSSSSGSAVAVCSGSGGVGVSAALAAVARGAGMGWGAAGSRAVS 644
QY 185 AACCGGTGTGGAGCGGTTCGCGCGCAAGTCTCGGCATCTTCACCGCGCAGTATCA 244
Db 645 AAASAAASSASSAASVVGAAACSSGSGSAGSSSAGAAARACASVCASSASSSGSCGSSSM 704
QY 245 CCGCGGTGACGCGGCTCCGATCACTCGGCCACCGGATGGCGGACGCGCTTAACGGCG 304
Db 705 CSAVSSGAASSGASGCGCGSSSSGSCSSSSMSCSSSSSSCSSSSGSCSCSCVSS 764
QY 305 ATCATCCCGGTGACGTATCTCGGTGACCTTGGCAAAACCAAGTCGGCGGACGCGTACAG 364
Db 765 CSSCSBSSCCSASSSRASSSSSSSSSSSSSVSCSMGCMAMSSASSASSSSSAGSSG 824

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QY 365 GGAACGTGACA 375
Db 825 SVVACGAVV 835

RESULT 26
BX456467
LOCUS
DEFINITION BX456467 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP002YE11
5-PRIME, mRNA sequence.
ACCESSION BX456467
VERSION BX456467
KEYWORDS BX456467.1 GI:31032763
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1200)
Li,W.B., Gruber,C., Jessee,J., and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP002AC06Q1.
Location/Qualifiers
FEATURES
source
1..1200
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP002YE11"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 11.3%; Score 44.6; DB 13; Length 1200;
Best Local Similarity 40.2%; Pred. No. 71;
Matches 103; Conservative 28; Mismatches 125; Indels 0; Gaps 0;
QY 5 CCGGTCGATGATCCAGCTGTCACAGGTGGGAGGATTCGCATTCGGATCGGC 64
Db 918 CCGGTCGATGATCCAGCTGTCACAGGTGGGAGGATTCGCATTCGGATCGGC 64
QY 65 AGGCGATGCGATCGCGGCGCAGATCCGATCGGTTGGGGGTACCCACGCTTCATATCG 124
Db 978 MRGCGGGGGCCCGSCCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 1037
QY 125 GGCCTACCGCTTCTCGGCTTGGTGTGTCGACAAACGACGAGCGCAGATGCC 184
Db 1038 SCGCCCCCGGSCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1097
QY 185 AACCGGTGTCTGGGAGCGCTCCGCGGCAAGTCTCGGATCTCCACCGGCGACGTGATCA 244
Db 1098 CCCCCCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1157
QY 245 CCGCGGTGACGGCGC 260
Db 1158 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1173

RESULT 27
BX360624/c
LOCUS
DEFINITION BX360624 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI072YL05 3-PRIME, mRNA sequence.
ACCESSION BX360624
VERSION BX360624.1 GI:30376452
KEYWORDS EST.
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J., and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI072CF03NP1.
Location/Qualifiers
FEATURES
source
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI072YL05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 11.3%; Score 44.6; DB 13; Length 1201;
Best Local Similarity 10.2%; Pred. No. 71;
Matches 19; Conservative 112; Mismatches 56; Indels 0; Gaps 0;
QY 94 TCGGTGGGGGTACCCACCGTTCATATCGGCGCTACCGCTTCCTCGGCTGGGTGT 153
Db 1090 TCGTWTGCSBBSCTTCTCCTCTCCTCTCCTCTCCTCTCCTCTCCTCTCCT 1031
QY 154 GTGCAACAAACGCAACGCGCAGTCCAAACGCTGTCGGAGGCGCTCCGCGGCA 213
Db 1030 STBBSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 971
QY 214 AGTCTCGGATCTCCACCGCGACGTGATCACCCTGCGGCGCTCGACGCGCTCACTCG 273
Db 970 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 911
QY 274 GCACCG 280
Db 910 SSSSVSS 904

RESULT 28
BX307565/c
LOCUS
DEFINITION BX307565 Y. Ogiwara unpublished cDNA library, wh_yl Triticum
aestivum cDNA clone whylp23 3', mRNA sequence.
ACCESSION BX307565
VERSION BX307565
KEYWORDS BX307565.1 GI:20116389
SOURCE EST.
ORGANISM Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 496)
Ogiwara,Y. and Murai,K.
Expressed genes in Triticum aestivum
TITLE

```

Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..496
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whydlp23"
/tissue types="spikelet at late flowering"
/dev stage="Feekes' scale 6"
/clone_lib="Y. Ogiwara unpublished cDNA library, Wh_yd"

ORIGIN
Query Match 11.2%; Score 44.4; DB 12; Length 496;
Best Local Similarity 49.2%; Pred. No. 64;
Matches 117; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 148 GGTGTTGTCGACAAACGCGGACGCGGACGAGTCCACGCGTGGTGGGAGCGGTCCG 207
Db 457 CTGGAGGTGATCACCACGCGACAGGTACAGAGCGGTCTCCACCGGTGGTGGCGAG 398
Qy 208 GCGGCAAGTCTCGGATCTCCACCGGACGAGTATACCGGCTGCGAGCGCGCTCCGATC 267
Db 397 GCCGACGCGAACCGGATGTCATCGCTCTTCTACCAACCGCGGACGCGGCTCATC 338
Qy 268 AACTCGGCCACCGGATCGCGGACGCGGTTAAACGGGATCATCCCGGTGAGCTCATCTCG 327
Db 337 TTCCCGCGCGCGCTCGCGGAGCGCGCGGCTGGTGGTACCCAGGTTGGTTCGAG 278
Qy 328 GTGACCTCGCAACCAAGTCTCGCGGACGCGTACAGGAACTGATTCGATTCGCGAGG 385
Db 277 GACTACATGAAGCTGTACGTGCGGCACCAAGTTCGATGACAGGACCGCGGTTGAGG 220

RESULT 29
BH190076/c
LOCUS
DEFINITION
ATXOC60TF ATXO Arabidopsis thaliana genomic clone ATXOC60, genomic survey sequence.
ACCESSION
BH190076
VERSION
BH190076.1 GI:16302878
KEYWORDS
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 504)
Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V., Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T24G4
Unpublished (2001)
Other_GSSs: ATXOC60TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1142. Caution: the DNA in this BAC may be from some non-Arabidopsis source
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..504
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="ATXO"
/note="Vector: PHOS2; Site 1: BstXI; 2-3 kb sheared BAC DNA inserted into PHOS2 using BstXI linkers"

FEATURES
source
1..504
Location/Qualifiers
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/strain="Columbia"
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/clone_lib="ATXO"
/note="Vector: PHOS2; Site 1: BstXI; 2-3 kb sheared BAC DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match 11.2%; Score 44.4; DB 28; Length 504;
Best Local Similarity 53.4%; Pred. No. 64;
Matches 93; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 155 TCGACACACGCGCAACGCGGACGAGTCCACCGCTGGTTCGAGCGGCTCCGCGGCAA 214
Db 401 TCGGTTTCGAGTCTATCGGATGACCAACCTCCCGAAGCCAACTCCCGCGAAGCGG 342
Qy 215 GTCTCGGATCTCCACCGGCGACGCTGATCACCGGCTGACGCGGCTCCGATCAACTCGG 274
Db 341 AGATCGCCTCGCCACCTCTCGCATGATCACCGACTACGCTGTGGAAAAACGACGAAG 282
Qy 275 CCACCGCATGCGGACGCGGTTTAAACGGGATCATCCCGGTGAGCTCATCTCGG 328
Db 281 CCCCCGTACCGCGCGAAGCGGCTGATCGCCCACTCCACGCAATGTACGATGG 228

Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..496
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whydlp23"
/tissue types="spikelet at late flowering"
/dev stage="Feekes' scale 6"
/clone_lib="Y. Ogiwara unpublished cDNA library, Wh_yd"

ORIGIN
Query Match 11.2%; Score 44.4; DB 12; Length 496;
Best Local Similarity 49.2%; Pred. No. 64;
Matches 117; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 148 GGTGTTGTCGACAAACGCGGACGCGGACGAGTCCACGCGTGGTGGGAGCGGTCCG 207
Db 457 CTGGAGGTGATCACCACGCGACAGGTACAGAGCGGTCTCCACCGGTGGTGGCGAG 398
Qy 208 GCGGCAAGTCTCGGATCTCCACCGGACGAGTATACCGGCTGCGAGCGCGCTCCGATC 267
Db 397 GCCGACGCGAACCGGATGTCATCGCTCTTCTACCAACCGCGGACGCGGCTCATC 338
Qy 268 AACTCGGCCACCGGATCGCGGACGCGGTTAAACGGGATCATCCCGGTGAGCTCATCTCG 327
Db 337 TTCCCGCGCGCGCTCGCGGAGCGCGCGGCTGGTGGTACCCAGGTTGGTTCGAG 278
Qy 328 GTGACCTCGCAACCAAGTCTCGCGGACGCGTACAGGAACTGATTCGATTCGCGAGG 385
Db 277 GACTACATGAAGCTGTACGTGCGGCACCAAGTTCGATGACAGGACCGCGGTTGAGG 220

RESULT 29
BH190076/c
LOCUS
DEFINITION
ATXOC60TF ATXO Arabidopsis thaliana genomic clone ATXOC60, genomic survey sequence.
ACCESSION
BH190076
VERSION
BH190076.1 GI:16302878
KEYWORDS
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 504)
Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V., Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T24G4
Unpublished (2001)
Other_GSSs: ATXOC60TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1142. Caution: the DNA in this BAC may be from some non-Arabidopsis source
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..504
/organism="Arabidopsis thaliana"

FEATURES
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1..504
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="ATXO"
/note="Vector: PHOS2; Site 1: BstXI; 2-3 kb sheared BAC DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match 11.2%; Score 44.4; DB 28; Length 590;
Best Local Similarity 53.4%; Pred. No. 66;
Matches 93; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 155 TCGACACACGCGCAACGCGGACGAGTCCACCGCTGGTTCGAGCGGCTCCGCGGCAA 214

Db	216	TCGGCTTCGACGTATCGGCATGACCAACCTCCCGAAGCAAGCTCGCCCGGAAGCG	157
Qy	215	GTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTGACGGCGCTCCGATCAACTCG	274
Db	156	AGATCGCCCTCGCCACCCCTCGCCATGATCACCGACTACCGACTCTGGAACCGACGAAG	97
Qy	275	CCACCGGATGGCGGACCGGCTTAAGGGCATCATCCCGTGACGTCACTCG	328
Db	96	CCCCCGTCACCGCGGAAGCGTCATCGCCCACTCCACGAAATGTCAGCATGG	43

Search completed: April 30, 2004, 07:40:32
Job time : 2052 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 20:30:12 ; Search time 364.086 Seconds

(without alignments)
1493.479 Million cell updates/sec

Title: US-09-684-215B-18

Perfect score: 653
Sequence: 1 TAASDNFQLSQGGGFAIP1.....QTKSGGTRTGNVLAEGPPA 128

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq_29Jan04 -QFT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09684215 @CEN 1.1.819 @runat_29042004_061304_13179 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_29Jan04: *
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2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002s: *
7: geneseqn2003as: *
8: geneseqn2003bs: *
9: geneseqn2003cs: *
10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	675	4	Aah93896 Ral2-P510
2	653	100.0	675	4	Aas64132 Human /M.
3	653	100.0	675	5	Acas59940 Prostate
4	653	100.0	675	5	Ab195503 Ral2- P51
5	653	100.0	675	7	ACC95667 Prostate
6	653	100.0	675	9	ADB14272 Human pro
7	653	100.0	675	9	Abk39769 DNA encod
8	653	100.0	822	7	ACA12098 Human lun

9	653	100.0	822	7	ACA03284	ACA03284 Lung canc
10	653	100.0	894	6	ABK27798	ABK27798 Human col
11	653	100.0	900	6	ABL49257	ABL49257 Ral2/C-te
12	653	100.0	900	6	ABQ92443	ABQ92443 Human lun
13	653	100.0	900	8	ADA28443	ADA28443 Lung tumo
14	653	100.0	915	4	AH93905	Ah93905 Ral2-P775
15	653	100.0	915	4	AAS64141	Aas64141 Human /M.
16	653	100.0	915	5	ACAS5949	Acas5949 Prostate
17	653	100.0	915	6	ABU95512	AB195512 Ral2- P77
18	653	100.0	915	7	ACC95676	Acc95676 Prostate
19	653	100.0	915	9	ADB14284	ADB14284 Human pro
20	653	100.0	945	6	ABK39768	Abk39768 DNA encod
21	653	100.0	945	7	ACA12097	ACA12097 Human lun
22	653	100.0	945	7	ACA03283	ACA03283 Lung canc
23	653	100.0	1012	6	ABL49256	Ab149256 Ral2/N-te
24	653	100.0	1012	8	ADA28441	Ada28441 Lung tumo
25	653	100.0	1012	8	ABK69714	Abk69714 DNA encod
26	653	100.0	1035	6	ABK69714	Abk69714 Human col
27	653	100.0	1035	7	AB233699	Ab233699 Human RAI
28	653	100.0	1035	9	ADB67590	ADB67590 Human RAI
29	653	100.0	1155	6	ABK39775	Abk39775 DNA encod
30	653	100.0	1155	7	ACA12104	ACA12104 Human RAI
31	653	100.0	1155	7	ACA03290	ACA03290 Lung canc
32	653	100.0	1203	4	AH93917	Aah93917 Ral2-P501
33	653	100.0	1203	4	AAS64153	Aas64153 Human /M.
34	653	100.0	1203	5	ACA59961	Acas59961 Prostate
35	653	100.0	1203	6	ABL95524	Ab195524 Ral2-P501
36	653	100.0	1203	7	ACC95688	Acc95688 Prostate
37	653	100.0	1203	9	ADB14301	Abd14301 Human pro
38	653	100.0	1263	6	ABK69715	Abk69715 DNA encod
39	653	100.0	1263	9	ADB67591	ADB67591 Human RAI
40	653	100.0	1464	4	AH56353	Aah56353 DNA encod
41	653	100.0	1464	6	ABL92582	Ab192582 Chlamydia
42	653	100.0	1557	4	AH56341	Aah56341 DNA encod
43	653	100.0	1557	6	ABU92570	Ab192570 Chlamydia
44	653	100.0	1578	3	AAS64764	Aas64764 C. pneumo
45	653	100.0	1578	4	AH56267	Aah56267 Chlamydia

ALIGNMENTS

RESULT 1

AAH93896
ID AAH93896 standard; cDNA; 675 BP.

XX AC AAH93896;

XX AC (first entry)

DT 04-OCT-2001 (first entry)

DE Ral2-P510S-C construct cDNA sequence.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

XX cytostatic; gene therapy; metastasis; ss.

XX Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIYA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

XX Kalos MD, Fanger GF, Day CH, Retter MW, Stolk JA, Skeiky YAW;

XX Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,

PT

PT monitoring and treating prostate cancer in a patient and for use in
 PT vaccines.
 XX
 PS Claim 8; Page 492-493; 543pp; English.
 XX
 CC The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
 CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
 CC the antibodies are also used in the detection of cancer in a patient. (I)
 CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
 CC and (II) can be used in vaccines. The antibodies or (I) can be used for
 CC monitoring the progression of cancer in a patient. (I) and (II) can also
 CC be used to improve diagnostic and therapeutic methods for prostate
 CC cancer. They can indicate the level of metastasis as well as the prostate
 CC volume. AH93357 to AAH93944 and AAH0115 to AAH01318 represent
 CC polynucleotide and amino acid sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,71e-58 Length: 675
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x AAH93896 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGTTGGCGAGGATTCGCAATTCGATC 81
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGCAGCGGATGCGGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
 QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArgValGlnArgVal 60
 Db 142 GCCTTCTCGCTGGTGGTGTGTCTGACACACAGCGGCAACGCGGATTCACGCGT 201
 QY 61 ValGlySerAlaProAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTCGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACC 261
 QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGGCGCTCCGATCACTCGGCACCGGATGCGGAGCGGCTTAACGGGATCATCC 321
 QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCCGGCGGCGACGCGTACAGGAA 381
 QY 121 ThrIleAlaGluGlyProProAla 128
 Db 382 ACATGGCCGAGGAGACCCCGGCC 405

RESULT 2

AAH93896
 ID AAS64132 standard; cDNA; 675 BP.

XX AC AAS64132;

XX 29-JAN-2002 (first entry)

DT Human /M. tuberculosis Ra12 fusion protein RA12-P510S-C cDNA.

DE Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.

XX Homo sapiens.

OS

OS Microbacterium; tuberculosis.
 OS Synthetic.
 OS Chimeric.
 XX
 PN WO200173032-A2.
 XX
 XX 04-OCT-2001.
 PD
 XX
 XX 27-MAR-2001; 2001WO-US009919.
 XX
 PF 27-MAR-2001; 2000US-00536857.
 XX
 PR 09-MAY-2000; 2000US-00568100.
 PR 13-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00635215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 XX WPI: 2001-639232/73.
 DR P-PSDB; AAU69899.
 DR
 XX
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.
 PT
 XX Example 17; Page 532; 579pp; English.
 PS
 XX The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific polynucleotide of the invention
 XX
 SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,71e-58 Length: 675
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x AAS64132 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGTTGGCGAGGATTCGCAATTCGATC 81
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGCAGCGGATGCGGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
 QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArgValGlnArgVal 60
 Db 142 GCCTTCTCGCTGGTGGTGTGTCTGACACACAGCGGCAACGCGGATTCACGCGT 201

Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTCGGAGCGCTCCGGCGCAAGTCTCGGATCTCCACCGCGCATCATCCCGGTC 261
 Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAenGlyHisPro 100
 Db 262 GACGGCGCTCCGATCACTCGGCCACCGCGATGGCGGCGCTTAACGGGATCATCCC 321
 Qy 101 GlyAspValIleSerValThrTrpGlnThrIlySerGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGCGACGCGTACAGGGAACGTG 381
 Qy 121 ThrLeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCCGAGGACCCCGGCC 405
 RESULT 3
 ID ACA59940 standard; cDNA; 675 BP.
 AC ACA59940;
 DT 10-JUN-2003 (first entry)
 DE Prostate cancer therapy associated cDNA #647.
 KW prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA; Gene; ss.
 OS Homo sapiens.
 PN US2002192763-A1.
 XX 19-DEC-2002.
 XX 29-JUN-2001; 2001US-00895793.
 XX 04-OCT-1999; 99US-0157455P.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX (XUJJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
 XX WPI; 2001-245062/25.

PT Prostate specific protein and its encoding polynucleotide, useful for the
 treatment and diagnosis of prostate cancer.
 XX Example 17; SEQ ID NO 822; 85pp; English.
 CC The invention describes a fusion protein comprising at least one amino
 acid sequence of immunogenic portions of any of the 3 sequences not
 defined in the specification, or sequences having at least 70 or 90 %
 sequence identity to any one of the 3 sequences defined in the USPTO web
 site, which is encoded by any of the 4 nucleotide sequences not defined
 in the specification. The fusion protein, composition and methods are
 useful for diagnosing, preventing and/or treating cancer, particularly
 prostate cancer. The proteins are useful as markers to indicate the
 presence or absence of cancer. This sequence represents a prostate cancer
 therapy associated cDNA. Note: This sequence data for this patent did not
 form part of the printed specification, but was obtained in electronic
 format directly from the US patent office at
 cc seqdata.uspto.gov/sequence.html?DocID=US20020192763
 XX
 SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,718-58 Length: 675
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0
 US-09-684-215B-18 (1-128) x ACA59940 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPhedInLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 Db 22 ACGGCGCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCCGCAATCCGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGCAGCGCATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
 Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
 Db 142 GCCTTCCTCGGCTGGGTGTTCGACACACACACGCGGCGACGAGTCAACGCGGTG 201
 Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGCGATGATCATCCCGGTC 261
 Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGGCGCTCCGATCACTCGGCCACCGGATGGCGGACGCGCTTAACGGGATCATCCC 321
 Qy 101 GlyAspValIleSerValThrTrpGlnThrIlySerGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGCGACGCGTACAGGGAACGTG 381
 Qy 121 ThrLeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 4
 ID ABL95503 standard; cDNA; 675 BP.
 XX ABL95503;
 AC ABL95503;
 DT 29-AUG-2003 (revised)
 DT 19-JUL-2002 (first entry)
 XX
 DE Ral2- P510S-C construct cDNA sequence SEQ ID NO 822.
 XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 KW gene therapy; gene; ss.

OS Mycobacterium tuberculosis.
OS Homo sapiens.
OS Chimeric.
XX US200202248-A1.
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-00759143.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 10-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 10-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIANG/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer.
XX
XX Example 17; SEQ ID NO 822; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a cDNA
XX described in the invention. (Updated on 29-AUG-2003 to standardise OS
XX field)
XX
XX Sequence 675 BP; 162 A; 197 C; 126 T; 0 U; 0 Other;
XX
XX Alignment Scores: 2.71e-58 Length: 675
XX Pred. No.:

Score: 553.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-18 (1-128) x ABL95503 (1-675)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCGCGCTCCGATTAACCTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGCACGCGATGCGGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheIleuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTGGGTGTGTGCGAACAAACGCGACGGCGACGAGTCCAAACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGAGCTGATCACC GCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaAlaAsnGlyHisHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCACTCTCGTGACCTGGCAACCAAGTCGGCGGCGCACCGGTACAGGAACGTG 381
QY 121 ThrIleAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405
RESULT 5
ACC95667
ID ACC95667 standard; cDNA; 675 BP.
XX
XX ACC95667;
XX
XX 28-AUG-2003 (first entry)
XX
XX Prostate tumour specific cDNA sequence SEQ ID 822.
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200289747-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002WO-US014753.
XX
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe Y;
XX Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
XX particularly for stimulating an immune response in a patient, or treating

```
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX Example 17; Page 601-602; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,71e-58 Length: 675
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-18 (1-128) x ACC95667 (1-675)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGCTGGCGAGGATTCCGCAATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGGGCGAGATCAAGCTTCCACCGTTCATATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGGCTTGGTGTGTGTCACAAACACGCGCAACGCGCGACGATCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCGGAGCGCTCCGGCGGCAAGTCTCGGATCTCCACCGCGAGCTGATCACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisIlePro 100
DB 262 GACGCGGCTCCGATCAACTCGGCCACCGCGATGGCGGAGCGGCTTAACGGGCATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCATCTCGGTACCTGGCAACCAACCAAGTCCGGCGGACCGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGGAGGACCCCGCGCC 405

RESULT 6
ADBI4272
ID ADBI4272 standard; cDNA; 675 BP.
XX
XX ADBI4272;
AC
XX
XX 18-DEC-2003 (first entry)
DT
DE Human prostate specific protein P510S-RA12 construct C cDNA.
XX
XX Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell; gene; fusion protein.
XX
XX Chimeric.
OS Homo sapiens.
OS Mycobacterium tuberculosis.
XX
XX US2003185830-A1.
XX
```

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PD 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806039.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 98US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 03-MAY-2002; 2002US-00144678.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
PI
XX
XX WPI: 2003-756193/71.
XX P-PSDB; ADBI4275.
XX
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 17; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
```

CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a cDNA encoding a
CC fusion protein comprising a prostate specific protein. Note: Except where
CC otherwise indicated, the sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,71e-58 Length: 675
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-18 (1-128) x ADBI4272 (1-675)
QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCGTGGCAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATTCGGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCTCTCGGCTGGGTGTGTGCACAAACACGCGACGCGAGTCCACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGAGTCTCGCATCTCCACCGCGAGTCAACGCGGTG 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGCGCGTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGCGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GTGACGTCATCTCGGTGACCTGGCAACCAACCAAGTCCGGCGGACGCGTACAGGAGCGTG 381

RESULT 7
ABK39769
ID ABK39769 standard; cDNA; 822 BP.
XX
AC ABK39769;
XX
XX 21-MAY-2002 (first entry)
XX
DE DNA encoding lung tumour protein P801P ORF5 and Ral2 fusion protein.
XX
XX Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
KW gene; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200204514-A2.
FN
XX
XX 17-JAN-2002.
PD
XX
XX 10-JUL-2001; 2001WO-US022058.
PF
XX
XX 11-JUL-2000; 2000US-00614124.
PR

PR 29-AUG-2000; 2000US-00651563.
PR 08-SEP-2000; 2000US-00658824.
PR 26-SEP-2000; 2000US-0087125.
PR 06-OCT-2000; 2000US-00677415.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.
XX
PA (CORI-) CORIXA CORP.
XX
XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marnerakis M, Carter D, Fanger GR, Vedvick JS, Bangur CS, McNabb A;
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX
DR WPI; 2002-164634/21.
DR P-PSDB; AAU55587.
XX
PT Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.
XX
XX Example 8; SEQ ID NO 1862; 223pp; English.
XX
CC The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumor protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumour
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumour protein.
CC This sequence encodes a lung tumour associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,44e-58 Length: 822
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x ABK39769 (1-822)
QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATTAACCTTCAGCTGTCCAGGCGTGGCAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATTCGGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCTCTCGGCTGGGTGTGTGCACAAACACGCGACGCGAGTCCACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGAGTCTCGCATCTCCACCGCGAGTCAACGCGGTG 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGCGCGTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGCGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GTGACGTCATCTCGGTGACCTGGCAACCAACCAAGTCCGGCGGACGCGTACAGGAGCGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128

CC treating a cancer in a patient (particularly lung cancer). The
CC oligonucleotide is useful for determining the presence of a cancer in a
CC patient. The protein and oligonucleotides are useful in pharmaceutical
CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
CC or primer for nucleic acid hybridisation, and in the design and
CC preparation of ribozyme molecules for inhibiting expression of the
CC polypeptides and proteins in tumour cells. An amplified portion of the
CC polynucleotide is useful for isolating a full-length gene from a suitable
CC library. The present sequence encodes a fusion protein of human RA12 with
CC the protein product of a cDNA (full length, extended or partial) isolated
CC from a library derived from lung tumour/cancer cells. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20020197669
XX
XX SQ Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,446-58 Length: 822
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-18 (1-128) X ACA12098 (1-822)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGGCGGCTCGGATAACTTCCAGCTGTCCAGGGGTGGCAGGGATTCCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGGCGATGGCGATCGGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCTCTCGGCTTGGGTGTTCGACAAACACCGGCGGCGAGTGTACACCGCGTGC 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGGGCTCCGGCGGCGAAGTCTCGGCATCTCCACCGCGAGTGTATCACCGCGTGC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGGCGAGCGCGCTTAACGGGCATCATGCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCTATTCGGTGACCTGGCAACCAAGTTCGGGCGGCGACGGGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGAGGAGCCCGCGGCC 405

RESULT 9
ACA03284
ID ACA03284 standard; DNA; 822 BP.
XX
XX ACA03284;
XX
XX 22-MAY-2003 (first entry)
XX
XX Lung cancer therapyand diagnosis associated DNA #5.
XX
XX Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ds.
XX
XX Homo sapiens.
XX
XX US2002129552-A1.
XX
XX 21-NOV-2002.
XX

DB 382 ACATTGGCGAGGAGCCCGCGGCC 405
RESULT 8
ACA12098
ID ACA12098 standard; cDNA; 822 BP.
XX
XX ACA12098;
XX
XX 06-JUN-2003 (first entry)
XX
XX Human lung cancer protein L801P ORF5/RA12 fusion protein cDNA.
XX
XX Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
XX
XX T cell expansion; CD4; CD8; RA12; gene.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX US2002197669-A1.
XX
XX 26-DEC-2002.
XX
XX 03-MAY-2001; 2001US-00849626.
XX
XX 13-DEC-2000; 2000US-00736457.
XX
XX (BANG/) BANGUR C S.
XX
XX (FANG/) FANGER G R.
XX
XX (WANG/) WANG A.
XX
XX (WANG/) WANG T.
XX
XX (SWIT/) SWITZER A P.
XX
XX (MCNE/) MCNEILL P D.
XX
XX (CLAP/) CLAPPER J D.
XX
XX Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
XX
XX Clapper JD;
XX
XX WPI: 2003-352750/33.
XX
XX P-PSDB; ABU63562.
XX
XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
XX
XX detecting the presence of lung cancer in a patient, and in pharmaceutical
XX
XX compositions, e.g. vaccines, for treating lung cancer.
XX
XX Example 8; Page; 72pp; English.
XX
XX The invention relates to a polynucleotide encoding a lung tumour protein,
XX
XX comprising a sequence selected from any of the 14 sequences mentioned in
XX
XX the specification, or a sequence (S2) mentioned in specification,
XX
XX complement of S1, sequences consisting of at least 20 contiguous residues
XX
XX of S1, sequences that hybridise to S1, sequences having 75%, preferably
XX
XX 90%, identity to S1, or degenerate variants of S1. Also included are an
XX
XX isolated polypeptide (comprising a sequence (S3) selected from any one of
XX
XX the 4 amino acid sequences mentioned in the specification, a sequence
XX
XX encoded by the polynucleotide, or sequences having at least 70%,
XX
XX preferably 90%, identity to a sequence encoded by the polynucleotide), an
XX
XX expression vector comprising the polynucleotide operably linked to an
XX
XX expression control sequence, a host cell transformed or transfected with
XX
XX the vector, an isolated antibody (or its antigen-binding fragment) that
XX
XX specifically binds to the polypeptide, detecting the presence of a cancer
XX
XX in a patient, a fusion protein comprising the polypeptide, an
XX
XX oligonucleotide that hybridises to S1 under moderately stringent
XX
XX conditions, stimulating and/or expanding T cells specific for a tumour
XX
XX protein (comprising contacting T cells with the polynucleotide, protein
XX
XX or antigen-presenting cells, under conditions and for a time sufficient
XX
XX to permit the stimulation and/or expansion of T cells) and inhibiting the
XX
XX development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T
XX
XX cells isolated from a patient with the polynucleotide, protein or antigen
XX
XX presenting cells that express the polynucleotide, such that T cells
XX
XX proliferate, administering to the patient an effective amount of the
XX
XX proliferated T cells, and thus inhibiting the development of a cancer in
XX
XX the patient. The polynucleotide, protein and cells are useful in a
XX
XX composition for stimulating an immune response in a patient, and for

PF	10-JUL-2001; 2001US-00902941.	Db	322 GGTGAGTCATCTCGTGCCTGGCAACCAAGTCGGCGGACCGGTACAGGACGTCG 381
XX		QY	121 ThrLeuAlaGluGlyProProAla 128
PR	30-JUN-1999; 99US-00346492.	Db	382 ACATTGGCCGAGGAGGACCCCGGCC 405
PR	15-OCT-1999; 99US-00419356.		
PR	17-DEC-1999; 99US-00466867.		
PR	30-DEC-1999; 99US-00476300.		
PR	06-MAR-2000; 2000US-00519642.		
PR	22-MAR-2000; 2000US-00533077.		
PR	10-APR-2000; 2000US-00546259.		
PR	27-APR-2000; 2000US-00560406.		
PR	05-JUN-2000; 2000US-00599184.		
PR	11-JUL-2000; 2000US-00614124.		
PR	29-AUG-2000; 2000US-00651563.		
PR	08-SEP-2000; 2000US-00658824.		
PR	26-SEP-2000; 2000US-00671325.		
PR	06-OCT-2000; 2000US-00677419.		
PR	30-OCT-2000; 2000US-00702705.		
PR	13-DEC-2000; 2000US-00736457.		
PR	03-MAY-2001; 2001US-00849626.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;		
PI	Durham M, Carter D, Fanger GR, Vedrick TS, Bangur CS, McNabb A;		
XX			
XX	WPI; 2003-328427/31.		
XX			
PT	New polynucleotide, useful for preparing a composition for treating or		
PT	inhibiting development of cancer, e.g. lung cancer.		
XX			
PS	Example 8; SEQID NO 1862; 82pp; English.		
XX			
CC	The invention describes an isolated polynucleotide comprising one of 32		
CC	sequences, complement or degenerate variants of them. The polynucleotide		
CC	is useful for preparing a composition e.g. a vaccine or for gene therapy,		
CC	for treating or inhibiting development of cancer, e.g. lung cancer. This		
CC	sequence represents a polynucleotide associated with the compositions and		
CC	methods for the therapy and diagnosis of lung cancer		
XX			
XX	Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;		
SQ			
Alignment Scores:			
Pred. No.:	3,44e-58	Length:	822
Score:	653.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0
US-09-684-215b-18 (1-128) x ACA03284 (1-822)			
QY	1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20		
Db	22 ACGGCGCGTCCGATACCTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 81		
QY	21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40		
Db	82 GGGCAGCGCATGCGATCGCGGCGCAGATCAAGCTTCCACCGTTTCATATCGGGCGTACC 141		
QY	41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAsnGlyValGlnArgVal 60		
Db	142 GCCTTCTCGCTGGGTGGTGTTCGACACACGCGACACGCGCAGATTCACACCGCTG 201		
QY	61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80		
Db	202 GTGCGGAGCGCTCGCGGCGCAAGTCTCGCATCTCCACCGCGACGTGATCACCGCGTGC 261		
QY	81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100		
Db	262 GACGGCGCTCCGATCAACTCGGCACCGCATGCGGACCGCTTAACGGGCATATCC 321		
QY	101 GlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120		

Sequence 894 BP; 207 A; 269 C; 237 G; 181 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,8e-58 Length: 894
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0

PF 30-NOV-2001; 2001WO-US047576.
 XX 12-DEC-2000; 2000US-00735705.
 PR 07-MAY-2001; 2001US-00850716.
 PR 28-JUN-2001; 2001US-00897778.
 XX (CORI-) CORIXA CORP.
 XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 XX McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
 PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
 XX WPI; 2002-583465/62.
 DR P-PSDB; ABP61920.
 XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded by
 PT the polynucleotides, useful in pharmaceutical compositions such as
 PT vaccines and as markers to indicate the presence of lung cancer.
 XX
 XX Claim 8; Page 340-341; 381pp; English.
 XX The present invention describes isolated human lung carcinoma
 CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
 CC activity, and can be used in gene therapy and in vaccines. Compositions
 CC comprising (I) or (II) can be used for stimulating an immune response in
 CC a patient and for treating lung cancer in a patient. Oligonucleotides of
 CC (I) can be used for detecting the presence of a cancer in a patient, by
 CC obtaining a biological sample from the patient, contacting the biological
 CC sample with the oligonucleotides, detecting in the sample, an amount of
 CC polynucleotide that hybridizes to the oligonucleotide and comparing the
 CC amount of polynucleotide that hybridizes to the oligonucleotide to a
 CC predetermined cut-off value, and determining the presence of a cancer in
 CC the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
 CC vaccines. (I) is useful as a marker to indicate the presence or absence
 CC of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to
 CC ABP61992 represent sequences used in the exemplification of the present
 CC invention
 XX
 XX Sequence 900 BP; 219 A; 239 C; 246 G; 196 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 3.83e-58 Length: 900
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-684-215B-18 (1-128) x ABQ92443 (1-900)
 QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProLe 20
 Db 22 ACGCGCGCGTCCGATTAATTCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGATC 81
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGGCAGCGGATGCGATCGCGGCCAGATCAAGCTTCCACCGTTTATTCGGGCTACC 141
 QY 41 AlapheLeuGlyLeuGlyValValAspAsnAsnGlyValAsnGlyValGlnArgVal 60
 Db 142 GCCTTCTCGCTGGTGTGTGTCGACACACACGCGCAACGGCGCAGTCCACGCGTG 201
 QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTCGGGAGCGCTCGCGGGAAGTCTCGGATCTCCACCGGCGACGTGATCACCGGGTC 261
 QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGGCGCTCGATCAACTGGCCACCGCATGGCGGACGCGTTAACGGGCATATCC 321
 QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCTATCTCGTGACCTGGTCAAAACCAAGTCGGCGCGGCACGGGTACAGGAACGTG 381

QY 121 ThrIeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCGGAGGAGACCCCGGCC 405
 RESULT 13
 ADA28443
 ID ADA28443 standard; cDNA; 900 BP.
 XX ADA28443;
 AC ADA28443;
 XX 20-NOV-2003 (first entry)
 DT Lung tumour protein L763P C-terminal/Ra12 fusion DNA.
 XX cancer; lung cancer; gene therapy; vaccine; human;
 XX lung squamous cell carcinoma; gene; ss; ra12.
 KW Homo sapiens.
 OS US2003064947-A1.
 PN 03-APR-2003.
 XX 30-NOV-2001; 2001US-00007700.
 XX 18-MAR-1998; 98US-00040802.
 XX 27-JUL-1998; 98US-00123912.
 XX 22-DEC-1998; 98US-00221107.
 XX 02-APR-1999; 99US-00285479.
 XX 17-DEC-1999; 99US-00466396.
 XX 30-DEC-1999; 99US-00476496.
 XX 10-JAN-2000; 2000US-00480884.
 XX 22-FEB-2000; 2000US-00510376.
 XX 04-APR-2000; 2000US-00542615.
 XX 28-JUN-2000; 2000US-00606421.
 XX 02-AUG-2000; 2000US-00630940.
 XX 21-AUG-2000; 2000US-00643597.
 XX 15-SEP-2000; 2000US-00662786.
 XX 09-OCT-2000; 2000US-00685696.
 XX 12-DEC-2000; 2000US-00735705.
 XX 07-MAY-2001; 2001US-00850716.
 XX 28-JUN-2001; 2001US-00897778.
 XX (CORI-) CORIXA CORP.
 XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 XX McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
 XX Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
 XX WPI; 2002-540798/51.
 XX P-PSDB; ADA28444.
 XX New isolated polynucleotides and polypeptides useful for diagnosing,
 XX preventing and/or treating cancer, particularly lung cancer.
 XX Claim 8; Page 253; 296pp; English.
 XX The invention describes isolated polynucleotides and polypeptides useful
 CC for diagnosing, preventing and/or treating cancer, particularly lung
 CC cancer. A new isolated polynucleotide comprises: any of the 22 fully
 CC defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the
 CC specification; complements of the nucleotide sequences cited above; at
 CC least 10 contiguous residues of the nucleotide sequences cited above; a
 CC sequence that hybridise to any of the nucleotide sequences under highly
 CC stringent conditions; a sequence that is at least 75 or 90% identical to
 CC the above nucleotide sequences; or degenerate variants of the above
 CC nucleotide sequences. The composition and methods are useful in
 CC diagnosing, preventing and/or treating cancer, particularly lung cancer,
 CC in gene therapy and in vaccines. This sequence encodes a fusion protein
 CC of human lung tumour protein L673P C-terminal and Ra12.
 XX Sequence 900 BP; 219 A; 239 C; 246 G; 196 T; 0 U; 0 Other;
 SQ

Alignment Scores: 3.83e-58 Length: 900
Pred. No.: 653.00 Matches: 128
Score: 653.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-684-215B-18 (1-128) x ADA28443 (1-900)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCCGCTCCGATTAACCTCCAGCTGTCACAGGTGGCAGGATTCGCCATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGATCGGATCGGGCCAGATCAAGCTTCCACCGCGAGCTGATCACCGCGTC 261
Qy 41 AlaPheLeuGlyLeuGlyValValAlaAsnAsnGlyValAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTGGGTGTGTCGACAAACACGCGACGCGGATTAACGGGATCATCCC 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGCAAGTCTCGCATCTCCACCGCGAGCTGATCACCGCGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsnAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCCGGCGCGACCGGTACAGGAACTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 14
AAH93905
ID AAH93905 standard; cDNA; 915 BP.
AC AAH93905;
DT 04-OCT-2001 (first entry)
DE Ra12-P775P-ORF3 construct cDNA sequence.
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytosolic; gene therapy; metastasis; ss.
XX Homo sapiens.
XX WO200151633-A2.
XX 19-JUL-2001.
XX 16-JAN-2001; 2001WO-US001574.
XX 14-JAN-2000; 2000US-00483672.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX Wang A, Meagher MJ;
XX WPI; 2001-425873/45.
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.

Claim 8; Page 497-498; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytosolic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used to treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention

XX Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;
XX

Alignment Scores: 3.91e-58 Length: 915
Pred. No.: 653.00 Matches: 128
Score: 653.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-684-215B-18 (1-128) x AAH93905 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCCGCTCCGATTAACCTCCAGCTGTCACAGGTGGCAGGATTCGCCATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGATCGGATCGGGCCAGATCAAGCTTCCACCGCGAGCTGATCACCGCGTC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAlaAsnAsnGlyValAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTGGGTGTGTCGACAAACACGCGACGCGGATTAACGGGATCATCCC 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGCAAGTCTCGCATCTCCACCGCGAGCTGATCACCGCGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsnAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCCGGCGCGACCGGTACAGGAACTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 15
AAH93905
ID AAH93905 standard; cDNA; 915 BP.
XX AAH93905;
XX 29-JAN-2002 (first entry)
XX Human /M. tuberculosis Ra12 fusion protein RA12-P775P-ORF3 cDNA.
XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX Homo sapiens.
XX Microbacterium; tuberculosis.
XX Synthetic.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT PT monitoring and treating prostate cancer in a patient and for use in
PT PT vaccines.


```
XX PS Example 17; SEQ ID NO 834; 85pp; English.
XX CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the usPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docID=US20020192763
XX SQ Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,91e-58 Length: 915
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-684-215B-18 (1-128) x ACA59949 (1-915)
Qy 1 ThrAlaIaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle 20
Db 22 ACGCCCGCGTCCGATACCTCCACGCTGCCAGGTCGGCAGGATTCCGCATTCGCATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValH:slleGlyProThr 40
Db 82 GGGCAGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTGTGTCACAAACACGCAACCGCGCAGTCCACACGGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTGATCACGCGGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
Db 262 GACGCGCTCCGATCAACTCGGCCACCGCGATGCGGACGCGCTTAACGGGCGATCATCCC 321
Qy 101 GlyAspValIleSerValThrTriPglThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCATCTCGTGACCTGGCAACCAACCAAGTCGGCGGCGCACGCGTACAGGGAAGTG 381

Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 17
ABL95512
ID ABL95512 standard; cDNA; 915 BP.
XX AC ABL95512;
XX AC
XX DT 29-AUG-2003 (revised)
XX DT 19-JUL-2002 (first entry)
XX XX
DE Ra12- P775P-ORF3 construct cDNA sequence SEQ ID NO 834.
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Mycobacterium tuberculosis.
OS Homo sapiens.
```

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OS Chimeric.
XX US2002022248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001; 2001US-00759143.
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 10-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 18-NOV-1999; 99US-00439313.
XX 12-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 10-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETI/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Ranger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
DR New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer.
PS Example 17; SEQ ID NO 834; 87pp; English.
XX CC
XX CC The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a cDNA
XX described in the invention. (Updated on 29-AUG-2003 to standardise OS
XX field)
XX SQ Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,91e-58 Length: 915
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
```

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x ABL95512 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
 Db 82 GGGCAGGCGATGGCGATCGCGGCGAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
 Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
 Db 142 GCCITCTCTCGCTTGGGTGTGTGACAAACACGCGACGCGCAGTCCAGTCCAGCGGTG 201
 Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTGGGAGCGCTCCGCGGCGAAGTCTCGGCATCTCCACCGCGCGATCACCGCGGTC 261
 Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGCGCTCCGATCAACTCGGCCACCGCGATGGCGAGCGGCTTAACGGGCGATCATCCC 321
 Qy 101 GlyAspValIleSerValThrTropGlnThrIlysserGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGCGCACGCGGTACAGGGAACGTG 381
 Qy 121 ThrLeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 18

ACC95676

ID ACC95676 standard; cDNA; 915 BP.

XX AC ACC95676;
 XX DT 28-AUG-2003 (first entry)
 XX DE Prostate tumour specific cDNA sequence SEQ ID 934.
 XX KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 XX KW immune response; prostate cancer; ss.

XX OS Homo sapiens.

XX PN WO200289747-A2.

XX PD 14-NOV-2002.

XX PF 09-MAY-2002; 2002WO-US014753.

XX PR 09-MAY-2001; 2001US-00852911.

XX PR 29-JUN-2001; 2001US-00895814.

XX PR 10-DEC-2001; 2001US-00012896.

XX PA (CORI-) CORIXA CORP.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick IS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De BassolisC, Foy TM, Watanabe Y;
 PI Deng T;

XX WI; 2003-167130/15.

XX New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.

XX

PS Example 17; Page 605-606; 691pp; English.

CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention

SQ Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,918-58 Length: 915
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-684-215B-18 (1-128) x ACC95676 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
 Db 82 GGGCAGGCGATGGCGATCGCGGCGAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
 Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
 Db 142 GCCITCTCTCGCTTGGGTGTGTGACAAACACGCGACGCGCAGTCCAGTCCAGCGGTG 201
 Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTGGGAGCGCTCCGCGGCGAAGTCTCGGCATCTCCACCGCGCGATCATCACCGCGGTC 261
 Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGCGCTCCGATCAACTCGGCCACCGCGATGGCGAGCGGCTTAACGGGCGATCATCCC 321
 Qy 101 GlyAspValIleSerValThrTropGlnThrIlysserGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGCGCGCACGCGGTACAGGGAACGTG 381
 Qy 121 ThrLeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 19

ADB14284

ID ADB14284 standard; cDNA; 915 BP.

XX AC ADB14284;

XX DT 18-DEC-2003 (first entry)

XX DE Human prostate specific protein P775P-ORF3-RA12 construct cDNA.
 XX KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
 KW gene therapy; cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell; gene; fusion protein.

XX OS Chimeric.

XX OS Homo sapiens.

XX OS Mycobacterium tuberculosis.

XX PN US2003185830-A1.

XX PD 02-OCT-2003.

XX

PF 12-NOV-2002; 2002US-00294025.
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Stolk JA, Kalos MD;
PI
XX WPI; 2003-756193/71.
DR P-PSDB; ADB14285.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Example 17; Page; 101pp; English.
XX
CC The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB13558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumor protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC

CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a cDNA encoding a
CC fusion protein comprising a prostate specific protein. Note: Except where
CC otherwise indicated the sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format.
CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3,91e-58 Length: 915
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-684-215B-18 (1-128) x ADB14284 (1-915)
QY 1 ThrAlaAlaSerAspAsnPhcInleuSerGInGlyGlyGInGlyPheAlaIleProIle 20
Db 22 ACGGGCGGCTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGGGATCCCATTCGGATC 81
QY 21 GlyGInAlaMetAlaIleAlaGlyGInIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAsnGlyAlaArgValGlnhArgVal 60
Db 142 GCCTTCTCGGCTGGGTGTTCGACCAACACGCGACGCGCGACGATCCCAACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTGATCACC GGCGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
Db 262 GACGGCGCTCCGATCAACTCCGCGCCACCGCGATGGGGAGCGCGCTTAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGInThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGGTGACCTGGCNAACCAAGTGGGGGGCGCGGTACAGGGACGTTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGAGACCCCGGCC 405
RESULT 20
ABK39768
ID ABK39768 standard; cDNA; 945 BP.
XX
AC ABK39768;
XX
DT 21-MAY-2002 (first entry)
XX
DE DNA encoding lung tumour protein P801P ORF4 and Rai2 fusion protein.
XX Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
KW gene; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200204514-A2.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US022058.
XX
PR 11-JUL-2000; 2000US-00614124.
PR 29-AUG-2000; 2000US-00651563.
PR 08-SEP-2000; 2000US-00658824.
PR

PR 26-SEP-2000; 2000US-00671325.
PR 06-OCT-2000; 2000US-00677419.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.
XX (CORI-) CORIXA CORP.
XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Mannerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX WPI; 2002-164634/21.
DR P-PSDB; AAU85586.
XX Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.
XX Example 8; SEQ ID NO 1861; 223pp; English.
PS The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumor protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumor
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumor protein.
CC This sequence encodes a lung tumor associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 945 BP; 150 A; 318 C; 360 G; 117 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,06e-58 Length: 945
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x ABK39768 (1-945)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCGAGGTGGCGAGGATTCGCAATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleLeuProThr 40
Db 82 GGGCAGCGGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAlaPheAsnAenGlyAenGlyValGlnArgVal 60
Db 142 GCGTTCCTCGGTGTTGTTCGACAAACACCGGACGCGGCGAGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGCAAGTCTCGCATCTCCACCGGCGAGTGCATACCGCGTCC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCACTCACTCGGCCACCGCGAGTGGCGGCGCGCTTAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGTCTATCTCGTGACCTGGCAACCAAGTCCGGCGGCGACCGGTACAGGACCGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGAGCCCGCGCC 405

RESULT 21
ACAI2097
ID ACAI2097 standard; cDNA; 945 BP.
XX ACAI2097;
AC ACAI2097;
XX 06-JUN-2003 (first entry)
XX Human lung cancer protein L801P ORF4/Ra12 fusion protein cDNA.
DE Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
KW T cell expansion; CD4; CD8; RA12; gene.
XX Homo sapiens.
OS Synthetic.
PN US2002197669-A1.
XX 26-DEC-2002.
XX 03-MAY-2001; 2001US-00849626.
XX 13-DEC-2000; 2000US-00736457.
PR (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
XX Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
PI Clapper JD;
XX WPI; 2003-352750/33.
DR P-PSDB; ABU69561.
XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
PT detecting the presence of lung cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating lung cancer.
XX Example 8; Page; 72pp; English.
XX The invention relates to a polynucleotide encoding a lung tumour protein,
CC comprising a sequence selected from any of the 14 sequences mentioned in
CC the specification, or a sequence (S2) mentioned in specification,
CC complement of S1, sequences consisting of at least 20 contiguous residues
CC of S1, sequences that hybridise to S1, sequences having 75% preferably
CC 90%, identity to S1, or degenerate variants of S1. Also included are an
CC isolated polypeptide (comprising a sequence (S3) selected from any one of
CC the 4 amino acid sequences mentioned in the specification, a sequence
CC encoded by the polynucleotide, or sequences having at least 70%,
CC preferably 90%, identity to a sequence encoded by the polynucleotide), an
CC expression vector comprising the polynucleotide operably linked to an
CC expression control sequence, a host cell transformed or transfected with
CC the vector, an isolated antibody (or its antigen-binding fragment) that
CC specifically binds to the polypeptide, detecting the presence of a cancer
CC in a patient, a fusion protein comprising the polypeptide, an
CC oligonucleotide that hybridises to S1 under moderately stringent
CC conditions, stimulating and/or expanding T cells specific for a tumour
CC protein (comprising contacting T cells with the polynucleotide, protein
CC or antigen-presenting cells under conditions and for a time sufficient
CC to permit the stimulation and/or expansion of T cells) and inhibiting the
CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
CC cells isolated from a patient with the polynucleotide, protein or antigen
CC presenting cells that express the polynucleotide, such that T cells
CC proliferate, administering to the patient an effective amount of the
CC proliferated T cells, and thus inhibiting the development of a cancer in
CC the patient. The polynucleotide, protein and cells are useful in a
CC composition for stimulating an immune response in a patient, and for
CC treating a cancer in a patient (particularly lung cancer). The
CC oligonucleotide is useful for determining the presence of a cancer in a

CC patient. The protein and oligonucleotides are useful in pharmaceutical
CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
CC or primer for nucleic acid hybridisation, and in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and proteins in tumour cells. An amplified portion of the
CC polynucleotide is useful for isolating a full-length gene from a suitable
CC library. The present sequence encodes a fusion protein of human RAL2 with
CC the protein product of a cDNA (full length, extended or partial) isolated
CC from a library derived from lung tumour/cancer cells. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the USPTO at
CC seqdata.uspro.gov/sequence.html?DocId=20020197669
XX
SQ Sequence 945 BP; 150 A; 318 C; 360 G; 117 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,06e-58 Length: 945
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-18 (1-128) x ACA12097 (1-945)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGCGCGCTCCGATTAACCTTCCAGCTGCTCCAGGGTGGGAGGATTCGGCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGCGATGGCGATCGGGGCCAGATCAAGTTCACCGTTCATATCGGGCCCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGGCTTGGGTGTTCGACACACACGCGCAACGGCGCAGATCCACCGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCAGCGTATCACCGCGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAACTCGGCCCGCGATGGCGGCGGCGGCGGCGGCGGCGGCGG 321
QY 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTACGCTCATCTCGGTGACCTGGCAACCAAGTCCGGCGCGCAGCGGTACAGGGACGTG 381

RESULT 22
ACA03283
ID ACA03283 standard; DNA; 945 BP.
XX
AC ACA03283;
XX
DT 22-MAY-2003 (first entry)
XX
DE Lung cancer therapy and diagnosis associated DNA #4.
XX
KW Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN US2002172952-A1.
XX
PD 21-NOV-2002.
XX
PF 10-JUL-2001; 2001US-00902941.
XX

PR 30-JUN-1999; 99US-00346492.
PR 15-OCT-1999; 99US-00419356.
PR 17-DEC-1999; 99US-00468867.
PR 06-DEC-1999; 99US-00476300.
PR 06-MAR-2000; 2000US-00519642.
PR 22-MAR-2000; 2000US-00533077.
PR 10-APR-2000; 2000US-00546259.
PR 27-APR-2000; 2000US-00560406.
PR 05-JUN-2000; 2000US-00589184.
PR 11-JUL-2000; 2000US-00614124.
PR 29-AUG-2000; 2000US-00651563.
PR 08-SEP-2000; 2000US-00658824.
PR 26-SEP-2000; 2000US-00671325.
PR 06-OCT-2000; 2000US-00677419.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.
XX
XX (CORI-) CORIXA CORP.
XX
PI Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;
PI Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;
XX
XX WPI; 2003-328427/31.
XX
XX New polynucleotide, useful for preparing a composition for treating or
XX inhibiting development of cancer, e.g. lung cancer.
XX
XX Example 8; SEQID NO 1861; 82pp; English.

CC The invention describes an isolated polynucleotide comprising one of 32
CC sequences, complement or degenerate variants of them. The polynucleotide
CC is useful for preparing a composition e.g. a vaccine or for gene therapy,
CC for treating or inhibiting development of cancer, e.g. lung cancer. This
CC sequence represents a polynucleotide associated with the compositions and
CC methods for the therapy and diagnosis of lung cancer
XX
SQ Sequence 945 BP; 150 A; 318 C; 360 G; 117 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,06e-58 Length: 945
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-18 (1-128) x ACA03283 (1-945)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGCGCGCTCCGATTAACCTTCCAGCTGCTCCAGGGTGGGAGGATTCGGCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGCGATGGCGATCGGGGCCAGATCAAGTTCACCGTTCATATCGGGCCCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGGCTTGGGTGTTCGACACACACGCGCAACGGCGCAGATCCACCGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCAGCGTATCACCGCGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAACTCGGCCCGCGATGGCGGCGGCGGCGGCGGCGGCGGCGG 321
QY 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTACGCTCATCTCGGTGACCTGGCAACCAAGTCCGGCGCGCAGCGGTACAGGGACGTG 381

CC amount of polynucleotide that hybridises to the oligonucleotide to a
CC predetermined cut-off value, and determining the presence of a cancer in
CC the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
CC vaccines. (I) is useful as a marker to indicate the presence or absence
CC of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to
CC AP61992 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 1012 BP; 235 A; 289 C; 289 G; 199 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,41e-58 Length: 1012
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x ABQ92442 (1-1012)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 67 ACGCCGCGTCCGATTAACCTTCACGTGTCCAGGGTGGCAGGATTCGCCATTCGGATC 126
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 127 GGGCAGCGATGCGATCGCGGCGCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 186
Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 187 GCCTTCTCGCTGGGTGGTGTGTGCACACACAGCGCAACGGCGCAGTCCACCGCGTG 246
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 247 GTCGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACGGCGAGTGCACCGCGGTC 306
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 307 GACGCGCTCGATCACTCGGCCACCGCGATGCGGACGCGCTTAACGGCGCATATCCC 366
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 367 GGTGACGTCTCTCGTGGTACTGGCAACCAAGTGGCGGCGGCGGCGGCGGACGCGT 426

Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 427 ACATTGGCGGAGGACCCCGGCC 450

RESULT 25
ADA28441
ID ADA28441 standard; cDNA; 1012 BP.
XX
AC ADA28441;
XX

XX 20-NOV-2003 (first entry)
XX
XX Lung tumour protein L763P N-terminal/Rai2 fusion DNA.
DE

XX cancer; lung cancer; gene therapy; vaccine; human;
KW lung squamous cell carcinoma; gene; ss; Rai2.
XX
XX Homo sapiens.
XX
XX US2003064947-A1.
XX

PD 03-APR-2003.
XX
XX 30-NOV-2001; 2001US-00007700.
XX
XX 18-MAR-1998; 98US-00040802.
PR 27-JUL-1998; 98US-00123912.
PR 22-DEC-1998; 98US-00221107.
PR 02-APR-1999; 98US-00285479.

PR 17-DEC-1999; 99US-00466396.
PR 30-DEC-1999; 99US-00476496.
PR 10-JAN-2000; 2000US-00480884.
PR 22-FEB-2000; 2000US-00510376.
PR 04-APR-2000; 2000US-00542615.
PR 28-JUN-2000; 2000US-00606421.
PR 02-AUG-2000; 2000US-00630940.
PR 21-AUG-2000; 2000US-00643597.
PR 15-SEP-2000; 2000US-00662786.
PR 09-OCT-2000; 2000US-00685696.
PR 12-DEC-2000; 2000US-00735705.
PR 07-MAY-2001; 2001US-00850716.
PR 28-JUN-2001; 2001US-00897778.
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TW;
XX
XX WPI: 2003-540798/51.
DR P-FSDB; ADA28441.

XX New isolated polynucleotides and polypeptides useful for diagnosing,
PT preventing and/or treating cancer, particularly lung cancer.
XX
XX Claim 8; Page 251-252; 296pp; English.

XX The invention describes isolated polynucleotides and polypeptides useful
CC for diagnosing, preventing and/or treating cancer, particularly lung
CC cancer. A new isolated polynucleotide comprises: any of the 22 fully
CC defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the
CC specification; complements of the nucleotide sequences cited above; at
CC least 10 contiguous residues of the nucleotide sequences under highly
CC stringent conditions; a sequence that is at least 75 or 90% identical to
CC the above nucleotide sequences; or degenerate variants of the above
CC nucleotide sequences. The composition and methods are useful in
CC diagnosing, preventing and/or treating cancer, particularly lung cancer,
CC in gene therapy and in vaccines. This sequence encodes a fusion protein
CC of human lung tumour protein L673P N-terminal and Rai2.
XX
SQ Sequence 1012 BP; 235 A; 289 C; 289 G; 199 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,41e-58 Length: 1012
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x ADA28441 (1-1012)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 67 ACGCCGCGTCCGATTAACCTTCACGTGTCCAGGGTGGCAGGATTCGCCATTCGGATC 126

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 127 GGGCAGCGATGCGATCGCGGCGCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 186
Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 187 GCCTTCTCGCTGGGTGGTGTGTGCACACACAGCGCAACGGCGCAGTCCACCGCGTG 246

Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 247 GTCGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACGGCGAGTGCACCGCGGTC 306
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 307 GACGCGCTCGATCACTCGGCCACCGCGATGCGGACGCGCTTAACGGCGCATATCCC 366


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Qy 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120
Db 367 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCCGGCGGCACGGGTACAGGGAACGTG 426
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 427 ACATTGGCCGAGGACCCCGGCC 450
RESULT 26
ID ABK69714
ID ABK69714 standard; cDNA; 1035 BP.
AC ABK69714;
XX
XX 15-JUL-2002 (first entry)
XX
XX DNA encoding human Ral2/WT1-E.
XX Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response;
XX gene; ss.
XX Homo sapiens.
XX
XX WO200228414-A1.
XX
XX 11-APR-2002.
XX
XX 03-OCT-2001; 2001WO-US031139.
XX
XX 06-OCT-2000; 2000US-00684361.
XX
XX 09-OCT-2000; 2000US-00685830.
XX
XX 15-FEB-2001; 2001US-00785019.
XX
XX 24-AUG-2001; 2001US-00938864.
XX
XX (CORI-) CORIXA CORP.
XX (GATG/) GAIGER A.
XX
XX Gaiger A, Mcneill PD, Smithgall M, Moulton G, Vedvick TS;
XX Sleath PR, Mossman S, Evans L, Spies AG, Boydaton J;
XX
XX WPI; 2002-352217/38.
XX P-PSDB; ABG33391.
XX
XX Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
XX treating and diagnosing cancer in a patient.
XX
XX Claim 1; Page 240; 260pp; English.
XX
XX The invention relates to an isolated WT1 polynucleotide (I) and
XX polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are
XX used for treating and detecting cancer in a patient, and for stimulating
XX an immune response in patient. ABK69648-ABK69724 represent WT1 coding
XX sequences and PCR primers of the invention
XX
XX Sequence 1035 BP; 217 A; 355 C; 291 G; 172 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.53e-58 Length: 1035
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215b-18 (1-128) x ABK69714 (1-1035)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIlePro 20
Db 4 ACGGCCGCGTCCGATTAATCCAGCTGTCCCGGGTGGCGAGGATTCGCCATTCCGATC 63
Qy 21 GlyGlnAlaMetAlaIleAlaGlnIleLysLeuProThrValHisIleGlyProThr 40
```

```
Db 64 GGGCAGCGGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTCATATCGGGCTACC 123
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 124 GCCTTCTCTCGGCTTGGGTGTGTGACCAACACGCAACGGCGCACGAGTCCACCGCTG 183
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 184 GTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGAGTGATCACCGCGTC 243
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisIlePro 100
Db 244 GACGGCGCTCCGATCAACTCCGCCACCGCGATGGCGGACGGCTTAAACGGGATCATCCC 303
Qy 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120
Db 304 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCCGGCGGCACGCGTACAGGGAACGTG 363
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 364 ACATTGGCCGAGGACCCCGGCC 387
RESULT 27
ID ABZ33699
ID ABZ33699 standard; cDNA; 1035 BP.
XX
XX AC ABZ33699;
XX
XX 30-JAN-2003 (first entry)
XX
XX Human colon tumour cDNA for Ral2-C884P-PCR2 SEQ ID NO:1084.
XX
XX Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
XX tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.
XX Homo sapiens.
XX
XX WO200283070-A2.
XX
XX 24-OCT-2002.
XX
XX 09-APR-2002; 2002WO-US011475.
XX
XX 10-APR-2001; 2001US-00833263.
XX
XX 03-AUG-2001; 2001US-00922217.
XX
XX 19-DEC-2001; 2001US-00025380.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Lodes MJ, Secretist H, Benson DR, Meagher MJ, Stolk JA;
XX Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
XX Fanger GR, Vedvick TS, Carter D;
XX
XX WPI; 2003-067548/06.
XX P-PSDB; ABP55373.
XX
XX New polynucleotide, useful for the preparation of a composition for
XX stimulating an immune response against, or treating, cancer.
XX
XX Claim 1; Page 474-475; 537pp; English.
XX
XX The present invention describes compounds (I) for the immunotherapy and
XX diagnosis of colon cancer. Also described: (1) a method for detecting the
XX presence of cancer in a patient; (2) a method for stimulating and/or
XX expanding T cells specific for a tumour protein; (3) an isolated T cell
XX population comprising T cells prepared by the method of (2); (4) a method
XX for stimulating an immune response in a patient; (5) a method for
XX treating cancer in a patient; and (6) a method for inhibiting the
XX development of cancer in a patient. (I) have immunostimulant and
XX cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725
XX and ABP55343 to ABP55391 represent human colon cancer/tumour related
XX sequences used in the exemplification of the present invention
XX
```

SQ Sequence 1035 BP; 252 A; 247 C; 274 G; 262 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,53e-58 Length: 1035
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-684-215B-18 (1-128) x ABZ33699 (1-1035)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
 DB 22 ACGCGCGCTCCGATTAACCTTCAGCTGTCACAGGTTGGCAGGATTCGCCATTCGATC 81
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
 DB 82 GGCAGCGATGCGATCGCGGCCAGATCAAGCTTCCACCGCTTCATATCGGCGCTACC 141
 QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaValArgValGlnArgVal 60
 DB 142 GCCTTCTCGCTTGGTGTGTGCGACACACGCGACGCGCCAGATTCACACCGCTG 201
 QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 DB 202 GTCCGAGCGCTCCGCGCGCAAGTCTCGGCATCTCCACCGCGCAGCTGATCACCGCGCTC 261
 QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 DB 262 GACGCGCTCCGATCACTACCTCGGCACCGCATCGCGACGCGCTTACCGGCATCATCC 321
 QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
 DB 322 GGTGAGTCACTCTCGTGACCTGGCAACCAAGTCCGGGGGCACGGTACAGGGAACGTG 381
 QY 121 ThrIleuAlaGlyProProAla 128
 DB 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 28
 ADB67590
 ID ADB67590 standard; cDNA; 1035 BP.
 AC ADB67590;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 XX Human RA12/WT1 E fusion protein cDNA.
 XX
 KW Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
 KW antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
 KW leukaemia; antigen; ss; gene.
 XX
 OS Chimeric.
 OS Homo sapiens.
 OS Mycobacterium tuberculosis.
 XX
 XX US2003072767-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 24-AUG-2001; 2001US-00938864.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 PR 06-OCT-2000; 2000US-00684361.
 PR 09-OCT-2000; 2000US-00685830.
 PR 15-FEB-2001; 2001US-00785019.
 XX
 XX (GAIG/) GAIGER A.
 PA (MCNE/) MCNEILL P. D.
 PA (SMIT/) SMITHGALL M.

PA (MOUL/) MOULTON G.
 PA (VEDV/) VEDVICK T S.
 PA (SLEA/) SLEATH P R.
 PA (MOSS/) MOSSMAN S.
 PA (EVAN/) EVANS L.
 PA (SPIE/) SPIES A G.
 PA (BOYD/) BOYDSTON J.
 XX
 XX Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 XX
 DR MPI; 2003-605957/57.
 XX P-PSDB; ADB67593.
 XX
 XX Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
 PT detecting the presence of cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
 XX
 PS Claim 1; Page 145; 197pp; English.
 XX
 CC The invention relates to an isolated Wilm tumour (WT1) polynucleotide
 CC comprising a full length protein, truncated protein, mutated protein or
 CC fusion protein. Also included are the encoded WT1 proteins, expression
 CC vectors, host cells, antibodies, detecting the presence of a cancer in a
 CC patient by contacting a biological sample with a binding agent that binds
 CC to a WT1 protein, an oligonucleotide that hybridises to a WT1
 CC polynucleotide, stimulating and/or expanding T cells specific for a
 CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
 CC protein or antigen-presenting cells that express the WT1 protein, a
 CC composition (C1) comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
 CC presenting cells that express the WT1 protein, inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the WT1 polynucleotide, the WT1
 CC protein or antigen presenting cells that express the WT1 protein, such
 CC that T cell proliferate, administering the proliferated T cells to the
 CC patient, and thus inhibiting the development of a cancer in the patient)
 CC and a composition (C2) comprising a WT1 polypeptide resuspended in a
 CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
 CC sucrose, fructose and glucose, at a concentration of 7-13%, and
 CC optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
 CC and MPL-SE or Enhazyn). Also disclosed as anew are polypeptides
 CC comprising a variant of an immunogenic portion of WT1 polypeptides
 CC useful for stimulating immune response in a patient, and for treating
 CC cancer in a patient. The oligonucleotide is also useful for determining
 CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
 CC protein are useful in pharmaceutical compositions, e.g. vaccines. the WT1
 CC protein is useful as marker to indicate the presence or absence of a
 CC cancer. C1 is useful for inhibiting the development of a malignant
 CC disease in a patient, for preventing and treating metastatic diseases
 CC e.g. leukaemia and cancer, and for removing tumour cells from a
 CC biological sample. Ab (binding agent for the WT1 protein) is useful for
 CC detecting the presence of cancer in a patient. The present sequence
 CC encodes a Human WT1 fusion protein.
 XX
 SQ Sequence 1035 BP; 217 A; 355 C; 291 G; 172 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,53e-58 Length: 1035
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-684-215B-18 (1-128) x ADB67590 (1-1035)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
 DB 4 ACGCGCGCTCCGATTAACCTTCAGCTGTCACAGGTTGGCAGGATTCGCCATTCGATC 63
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40

PA (FANG/) FANGER G R.
 PA (WANG/) WANG A.
 PA (WANG/) WANG T.
 PA (SWIT/) SWITZER A P.
 PA (MCNE/) MCNEILL P D.
 PA (CLAP/) CLAPPER J D.
 XX

PI Bangor CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
 PI Clapper JD;
 XX

DR WPI: 2003-352750/33.
 DR P-PSDB; ABU69568.
 XX

XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
 PT detecting the presence of lung cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating lung cancer.
 XX

PS Example 10; Page; 72pp; English.
 XX

CC The invention relates to a polynucleotide encoding a lung tumour protein,
 CC comprising a sequence selected from any of the 14 sequences mentioned in
 CC the specification, or a sequence (S2) mentioned in specification,
 CC complement of S1, sequences consisting of at least 20 contiguous residues
 CC of S1, sequences that hybridise to S1, sequences having 75%, preferably
 CC 90%, identity to S1, or degenerate variants of S1. Also included are an
 CC isolated polypeptide (comprising a sequence (S3) selected from any one of
 CC the 4 amino acid sequences mentioned in the specification, a sequence
 CC encoded by the polynucleotide, or sequences having at least 70%,
 CC preferably 90%, identity to a sequence encoded by the polynucleotide), an
 CC expression vector comprising the polynucleotide operably linked to an
 CC expression control sequence, a host cell transformed or transfected with
 CC the vector, an isolated antibody (or its antigen-binding fragment) that
 CC specifically binds to the polypeptide, detecting the presence of a cancer
 CC in a patient, a fusion protein comprising the polypeptide, an
 CC oligonucleotide that hybridises to S1 under moderately stringent
 CC conditions, stimulating and/or expanding T cells specific for a tumour
 CC protein (comprising contacting T cells with the polynucleotide, protein
 CC or antigen-presenting cells, under conditions and for a time sufficient
 CC to permit the stimulation and/or expansion of T cells) and inhibiting the
 CC development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T
 CC cells isolated from a patient with the polynucleotide, protein or antigen
 CC presenting cells that express the polynucleotide, such that T cells
 CC proliferate, administering to the patient an effective amount of the
 CC proliferated T cells, and thus inhibiting the development of a cancer in
 CC the patient. The polynucleotide, protein and cells are useful in a
 CC composition for stimulating an immune response in a patient, and for
 CC treating a cancer in a patient (particularly lung cancer). The
 CC oligonucleotide is useful for determining the presence of a cancer in a
 CC patient. The protein and oligonucleotides are useful in pharmaceutical
 CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
 CC or primer for nucleic acid hybridisation, and in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the
 CC polypeptides and proteins in tumour cells. An amplified portion of the
 CC polynucleotide is useful for isolating a full-length gene from a suitable
 CC library. The present sequence encodes a fusion protein of human RAL2 with
 CC the protein product of a cDNA (full length, extended or partial) isolated
 CC from a library derived from lung tumour/cancer cells. Note: the sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from the USPTO at
 CC seqdata.uspto.gov/sequence.html?DocId=20020197669
 XX
 XX Sequence 1155 BP; 239 A; 346 C; 302 G; 268 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.17e-58	Length:	1155
Score:	653.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB:	7	Gaps:	0

US-09-684-215B-18 (1-128) x ACA12104 (1-1155)

Qy	1	ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle	20
Db	22	ACGCCCGCGTCGATRACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC	81
Qy	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuSerProThrValHisIleGlyProThr	40
Db	82	GGGCGAGCGGATGGCGATCGCGGCCAGATCAAGCTTCCACCCGTTCTATATCGGGCTACC	141
Qy	41	AlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal	60
Db	142	GCCTTCCTCGCTTGGGTGTGTGTCGACACACACGCGCAACGCGGCACGAGTCCACGCGGTG	201
Qy	61	ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal	80
Db	202	GTCGGGAGCGTTCGGCGGCAAGTCTCGGCATCTCCACCGCGCAGTGATCACCGCGGTC	261
Qy	81	AspGlyAlaProIleAsnSerAlaThrAlaValAlaAspAlaLeuAsnGlyHisHisPro	100
Db	262	GACGGCGCTCGGATCAACTCGGCCACCGCATGGCGGACGCGGCTTAACGGGCATCATCC	321
Qy	101	GlyAspValIleSerValThrTrpGlnThrIleSerSerGlyThrArgThrGlyAsnVal	120
Db	322	GGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCGGCGCGGACGCGTCACAGGAACTG	381
Qy	121	ThrLeuAlaGluGlyProProAla	128
Db	382	ACATTGGCGGAGGACCCCGGCC	405

Search completed: April 29, 2004, 23:03:11
 Job time : 368.096 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 20:32:52 ; Search time 3670.05 seconds
(without alignments)
1511.672 Million cell updates/sec

US-09-684-215B-18

Title: 653
Sequence: 1 TAAADNFQLSQGQGFAPL.....CAGGGTRGVNVLAEPPA 128

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -NATRIX=blotsum62 -TRANS=human40.cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
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7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
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14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_or.*
21: em_ov.*
22: em_pat.*
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25: em_ro.*
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29: em_vi.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	653	100.0	675	6	AR261272	Sequence
2	653	100.0	675	6	AR400535	Sequence
3	653	100.0	675	6	AR405802	Sequence
4	653	100.0	675	6	AX201049	Sequence
5	653	100.0	675	6	AX267848	Sequence
6	653	100.0	822	6	AR277645	Sequence
7	653	100.0	822	6	AX369152	Sequence
8	653	100.0	894	6	AX351489	Sequence
9	653	100.0	900	6	AR220690	Sequence
10	653	100.0	900	6	AX365960	Sequence
11	653	100.0	915	6	AR261281	Sequence
12	653	100.0	915	6	AR400544	Sequence
13	653	100.0	915	6	AR405811	Sequence
14	653	100.0	915	6	AX201061	Sequence
15	653	100.0	915	6	AX267860	Sequence
16	653	100.0	945	6	AR277644	Sequence
17	653	100.0	945	6	AX369151	Sequence
18	653	100.0	1012	6	AR220689	Sequence
19	653	100.0	1012	6	AX365958	Sequence
20	653	100.0	1155	6	AX369165	Sequence
21	653	100.0	1203	6	AR400556	Sequence
22	653	100.0	1203	6	AR405823	Sequence
23	653	100.0	1203	6	AX201078	Sequence
24	653	100.0	1203	6	AX267877	Sequence
25	653	100.0	1464	6	AR229410	Sequence
26	653	100.0	1464	6	AX322028	Sequence
27	653	100.0	1464	6	AX156105	Sequence
28	653	100.0	1464	6	AX361955	Sequence
29	653	100.0	1557	6	AR229398	Sequence
30	653	100.0	1557	6	AR322016	Sequence
31	653	100.0	1557	6	AX156089	Sequence
32	653	100.0	1557	6	AX361939	Sequence
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35	653	100.0	1578	6	AR321946	Sequence
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38	653	100.0	1590	6	AX316986	Sequence
39	653	100.0	1752	6	AR229413	Sequence
40	653	100.0	1752	6	AX322031	Sequence
41	653	100.0	1752	6	AX156109	Sequence
42	653	100.0	1752	6	AX361959	Sequence
43	653	100.0	1758	6	AR229401	Sequence
44	653	100.0	1758	6	AR322019	Sequence
45	653	100.0	1758	6	AX156093	Sequence

ALIGNMENTS

RESULT 1

AR261272 LOCUS AR261272 675 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 822 from patent US 6321716.
ACCESSION AR261272
VERSION AR261272.1 GI:28072035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Mashiki, Z. and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 822 27-NOV-2001;
FEATURES Location/Qualifiers
DB: 1..675
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.4e-44 Length: 675
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR261272 (1-675)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCGAGGATTCCGCATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCCGGGCGCAGATCAAGCTTCCACCGTTCATATCGGCGTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTTCGACAAACACGCGACGCGGATCCCAACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCACTCTCCACCGGCGAGTGATCACCGCGTGC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGCGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405

RESULT 2
AR400535 LOCUS AR400535 675 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 822 from patent US 6620922.
ACCESSION AR400535
VERSION AR400535.1 GI:40144000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

Cancer
Patent: US 6620922-A 822 16-SEP-2003;
JOURNAL Location/Qualifiers
FEATURES 1..675
source /organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.4e-44 Length: 675
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR400535 (1-675)
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Db 22 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCGAGGATTCCGCATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCCGGGCGCAGATCAAGCTTCCACCGTTCATATCGGCGTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTTCGACAAACACGCGACGCGGATCCCAACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCACTCTCCACCGGCGAGTGATCACCGCGTGC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGCGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405

RESULT 3
AR405802 LOCUS AR405802 675 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 822 from patent US 6630305.
ACCESSION AR405802
VERSION AR405802.1 GI:40154639
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6630305-A 822 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..675
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.4e-44 Length: 675
Score: 653.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR405802 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
 Db 22 ACGCCCGCTCCGATTAACCTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGGCAGCGGATGGGATCGCGGGCCAGATCAAGCTTCCAGCTTCATATCGGGCCATCC 141
 Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
 Db 142 GCTTCTCGCTGGCTTGGGTGTGTCGACACACGCAACGCGCACGAGTCCACGCGTG 201
 Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGCAGTGTACCGCGGTC 261
 Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGGCGCTCCGATCACTCGGCACCGCATGGCGACGCGCTTAACGGGCATCATCC 321
 Qy 101 GlyAspValIleSerValThrTrpGlnThrIlySerGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCTCTCGTGAACCTGCAACCAAGTCTGGCGGCGCAGTGTACAGGAACGTG 381
 Qy 121 ThrLeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 5
 AX267848 675 bp DNA linear PAT 26-OCT-2001
 LOCUS AX267848
 DEFINITION Sequence 822 from Patent WO0173032.
 ACCESSION AX267848
 VERSION AX267848.1 GI:16516494
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
 Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
 Vedwick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, F.A., Hepler, W.T.
 and Henderson, R.A.
 Compositions and methods for the therapy and diagnosis of prostate
 cancer
 Patent: WO 0173032-A 822 04-OCT-2001;
 CORIXA CORPORATION (US)

FEATURES
 source
 1. 675
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.4e-44 Length: 675
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX267848 (1-675)

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 Db 22 ACGCCCGCTCCGATTAACCTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGGCAGCGGATGGGATCGCGGGCCAGATCAAGCTTCCAGCTTCATATCGGGCCATCC 141
 Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR405802 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
 Db 22 ACGCCCGCTCCGATTAACCTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
 Db 82 GGGCAGCGGATGGGATCGCGGGCCAGATCAAGCTTCCACCGCTTCATATCGGGCCATCC 141
 Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
 Db 142 GCTTCTCGCTGGCTTGGGTGTGTCGACACACGCAACGCGCACGAGTCCACGCGTG 201
 Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
 Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGCAGTGTACCGCGGTC 261
 Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
 Db 262 GACGGCGCTCCGATCAACTCGGCACCGCATGGCGACGCGCTTAACGGGCATCATCC 321
 Qy 101 GlyAspValIleSerValThrTrpGlnThrIlySerGlyGlyThrArgThrGlyAsnVal 120
 Db 322 GGTGACGTCTCTCGTGAACCTGCAACCAAGTCTGGCGGCGCAGTGTACAGGAACGTG 381
 Qy 121 ThrLeuAlaGluGlyProProAla 128
 Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 4
 AX201049 675 bp DNA linear PAT 29-AUG-2001
 LOCUS AX201049
 DEFINITION Sequence 679 from Patent WO0151633.
 ACCESSION AX201049
 VERSION AX201049.1 GI:15390857
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
 Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
 Stolk, J.A., Skeiky, F.A., Wang, A. and Meagher, M.J.
 Compositions and methods for the therapy and diagnosis of prostate
 cancer
 Patent: WO 0151633-A 679 19-JUL-2001;
 CORIXA CORPORATION (US)

FEATURES
 source
 1. 675
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.4e-44 Length: 675
 Score: 653.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX201049 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20

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Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyLeuThrGlyAspValIleThrAlaVal 80

Db 202 GTCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTGATCACCGCGTC 261

Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100

Db 262 GACGGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGGCTTAACGGGCATCATCCC 321

Qy 101 GlyAspValIleSerValThrTripglnThrLysSerGlyGlyThrArgThrGlyAsnVal 120

Db 322 GGTGACGTCACTCGGTGACCTGGCAACACCAAGTCGGCGGCACGCGTACAGGAAACGTG 381

Qy 121 ThrLeuAlaGluGlyProProAla 128

Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 6

LOCUS AR277645 822 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 1862 from patent US 6509448.

ACCESSION AR277645

VERSION AR277645.1 GI:29711294

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 822)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: US 6509448-A 1862 21-JAN-2003;

FEATURES

source

1..822

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2,95e-44 Length: 822

Score: 653.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR277645 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

Db 22 ACGGGCGGCTCCGATAACTTCAGCTGCCAGGCTGGCGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTCATATCGGGCTACC 141

Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyValAlaArgValGlnArgVal 60

Db 142 GCCTTCCTCGGCTCCGATAACTTCAGCTGCCAGGCTGGCGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTCATATCGGGCTACC 141

Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyValAlaArgValGlnArgVal 60

Db 142 GCCTTCCTCGGCTCCGATAACTTCAGCTGCCAGGCTGGCGAGGATTCGCCATTCGGATC 81

Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80

Db 202 GTCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGTC 261

Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100

Db 262 GACGGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGGCTTAACGGGCATCATCCC 321

Qy 101 GlyAspValIleSerValThrTripglnThrLysSerGlyGlyThrArgThrGlyAsnVal 120

Db 322 GGTGACGTCACTCGGTGACCTGGCAACACCAAGTCGGCGGCACGCGTACAGGAAACGTG 381

Qy 121 ThrLeuAlaGluGlyProProAla 128

Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 7

LOCUS AX369152 822 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 1862 from Patent WO0204514.

ACCESSION AX369152

VERSION AX369152.1 GI:18857170

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W., Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S., Mcnabb, A., Fanger, N., Switzer, A., Mcneill, P.D. and Clapper, J.D.

TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: WO 0204514-A 1862 17-JAN-2002;

FEATURES

source

1..822

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 2,95e-44 Length: 822

Score: 653.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX369152 (1-822)

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Db 22 ACGGGCGGCTCCGATAACTTCAGCTGCCAGGCTGGCGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTCATATCGGGCTACC 141

Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyValAlaArgValGlnArgVal 60

Db 142 GCCTTCCTCGGCTCCGATAACTTCAGCTGCCAGGCTGGCGAGGATTCGCCATTCGGATC 81

Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80

Db 202 GTCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGTC 261

Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100

Db 262 GACGGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGGCTTAACGGGCATCATCCC 321

Qy 101 GlyAspValIleSerValThrTripglnThrLysSerGlyGlyThrArgThrGlyAsnVal 120

Db 322 GGTGACGTCACTCGGTGACCTGGCAACACCAAGTCGGCGGCACGCGTACAGGAAACGTG 381

Qy 121 ThrLeuAlaGluGlyProProAla 128

Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 8

LOCUS AX351489 894 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 236 from Patent WO0198390.

ACCESSION AX351489
VERSION AX351489.1 GI:18616835
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jiang Y., Hepler, W.T., Clapper, J.D., Wang, A. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0196390-A 236 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
source 1. 894
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3.21e-44 Length: 894
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-18 (1-128) x AX351489 (1-894)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGCTCCGATCAACTTCAGCTGCCAGGTCGGCAGGATTCCGCAATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTGGGTGTTCGACAAACACGCGCAGCAGTCCACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGAGCGCTCCGGCGGAGTCTCGCATCTCCACCGGCGAGTGCATCACCGGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisIlePro 100
Db 262 GACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGTCATCCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGTGACCTGGCAACCAAGTCGGGCGGCACCGGTACAGGAACTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405

RESULT 9
AX351489
LOCUS 900 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 353 from patent US 6426072.
ACCESSION AR220690
VERSION AR220690.1 GI:23327471
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 900)
AUTHORS Wang, T., Fan, L., Kalos, M.D., Bangur, C.S., Hosken, N.A., Fanger, G.R., Li, S.X., Wang, A., Skeiky, Y.A.W., Henderson, R.A., and McNeill, P.D.
TITLE Compositions and methods for the therapy and diagnosis of lung cancer

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGCTCCGATCAACTTCAGCTGCCAGGTCGGCAGGATTCCGCAATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTGGGTGTTCGACAAACACGCGCAGCAGTCCACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGAGCGCTCCGGCGGAGTCTCGCATCTCCACCGGCGAGTGCATCACCGGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisIlePro 100
Db 262 GACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGTCATCCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGTGACCTGGCAACCAAGTCGGGCGGCACCGGTACAGGAACTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405

RESULT 9
AX351489
LOCUS 900 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 353 from Patent WO0200174.
ACCESSION AX365960
VERSION AX365960.1 GI:18697458
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wang, T., Wang, A., Skeiky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A., McNeill, P.D., Fanger, N., Retter, M.W., Marnierakis, M., Fanger, G.R., Vedvick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.
TITLE Compositions and methods for the therapy and diagnosis of lung cancer
JOURNAL Patent: WO 0200174-A 353 03-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source 1. 900
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3.24e-44 Length: 900
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-18 (1-128) x AR220690 (1-900)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGCTCCGATCAACTTCAGCTGCCAGGTCGGCAGGATTCCGCAATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTGGGTGTTCGACAAACACGCGCAGCAGTCCACGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGAGCGCTCCGGCGGAGTCTCGCATCTCCACCGGCGAGTGCATCACCGGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisIlePro 100
Db 262 GACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGTCATCCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGTGACCTGGCAACCAAGTCGGGCGGCACCGGTACAGGAACTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405

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Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX365960 (1-900)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCCGGTCCGATCACTCCAGCTGCCAGGGTGGCGAGGATTCGGCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGCGGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGCTGGGTGTGTGTCACAAACACGCGGACCGGATTCACCGCGGTC 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGAGCGCTCCGGCGCAAGTCTCCACCGCGAGCGTATCACC CGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCACTCCGCCACCGGATGGCGGACGGCTTACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrIleLysSerGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCACTCGGTGACCTGGCAACCAAGTCCGGCGGCACGCTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 12
LOCUS AR400544 915 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 834 from patent US 6620922.
ACCESSION AR400544
VERSION AR400544.1 GI:40144016
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 915)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Ratter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 834 16-SEP-2003;
FEATURES Location/Qualifiers
source 1..915
/mol_type="genomic DNA"

ORIGIN
Alignment Scores: 3,29e-44 Length: 915
Pred. No.: 653.00 Matches: 128
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-684-215B-18 (1-128) x AR400544 (1-915)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCCGGTCCGATCACTCCAGCTGCCAGGGTGGCGAGGATTCGGCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGCGGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGCTGGGTGTGTGTCACAAACACGCGGACCGGATTCACCGCGGTC 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGAGCGCTCCGGCGCAAGTCTCCACCGCGAGCGTATCACC CGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 11
LOCUS AR261281 915 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 834 from patent US 6321716.
ACCESSION AR261281
VERSION AR261281.1 GI:28072044
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 915)
AUTHORS Mashiki, Z. and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 834 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..915
/mol_type="genomic DNA"

ORIGIN
Alignment Scores: 3,29e-44 Length: 915
Pred. No.: 653.00 Matches: 128
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-684-215B-18 (1-128) x AR261281 (1-915)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCCGGTCCGATCACTCCAGCTGCCAGGGTGGCGAGGATTCGGCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGCGGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
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Db 262 GACGGCGCTCCGATCACTCGGCCACCGCGATGGCGGCGCTTAACGGGCATCATCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCTCGGTGACCTCGCAACCAAGTCGGCGGCGACGGGTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 13
AR405811
LOCUS AR405811 915 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 834 from patent US 6630305.
ACCESSION AR405811
VERSION AR405811.1 GI:40154648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 915)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H., Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 834 07-OCT-2003;
FEATURES
source 1..915
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/mol_type="genomic DNA"

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Alignment Scores:
Pred. No.: 3,298-44 Length: 915
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCTCGGCTTGGGTGTTGTCGACAAACACGCGACGGCGACGAGTCCAAACGGGTG 201
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AX201061
LOCUS AX201061 915 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 691 from Patent WO0151633.
ACCESSION AX201061
VERSION AX201061.1 GI:15390868
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: WO 0151633-A 691 19-JUL-2001;
FEATURES
source 1..915
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCTCGGCTTGGGTGTTGTCGACAAACACGCGACGGCGACGAGTCCAAACGGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGAGTGTATCACCAGCGTGC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
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Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 15
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LOCUS AX267860 915 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 834 from Patent WO0173032.
ACCESSION AX267860
VERSION AX267860.1 GI:16516503
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hegler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate cancer

Patent: WO 0173032-A 834 04-OCT-2001;

CORIXA CORPORATION (US)

Location/Qualifiers

1. .945

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40

Db 82 GGGCAGGGCGATCGGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCCATCC 141

Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60

Db 142 GCCTTCCTCGCTTGGTGTTCGACACACGCGGACGCGGACGAGTCCACGCGTG 201

Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80

Db 202 GTCCGAGGCGTCCGCGGCAAGTCTCCGATCTCCACCGCGAGCTGATCACCAGCGGTC 261

Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100

Db 262 GACGCGCTCCGATCACTCGCCACCGGATGGCGGCGGCGGATTAACGGGCTATATCC 321

Qy 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120

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Qy 121 ThrLeuAlaGluGlyProProAla 128

Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 16

AR277644

LOCUS

Sequence 1861 from patent US 6509448.

ACCESSION

AR277644.1 GI:29711293

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S., Carter,D., Retter,M.W., Mannion,J., Fan,L. and Wang,A.

TITLE

Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL

Patent: US 6509448-A 1861 21-JAN-2003;

FEATURES

Location/Qualifiers

1. .945

source

ORIGIN

Alignment Scores:

Pred. No.: 3.41e-44 Length: 945

Score: 653.00 Matches: 128

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLeuProThrValHisIleGlyProThr 40

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Qy 41 AlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArgValGlnArgVal 60

Db 142 GCCTTCCTCGCTTGGTGTTCGACACACGCGGACGCGGACGAGTCCACGCGTG 201

Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80

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RESULT 17

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Sequence 1861 from Patent WO0204514.

ACCESSION

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VERSION

AX369151.1 GI:18857169

KEYWORDS

SOURCE

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W., Marnierakis,M., Carter,D., Fanger,G.R., Vedvick,T.S., Bangur,C.S., Mcnabb,A., Fanger,N., Switzer,A., Mcneill,P.D. and Clapper,J.D.

TITLE

Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL

Patent: WO 0204514-A 1861 17-JAN-2002;

FEATURES

Location/Qualifiers

1. .945

/organism="Homo sapiens"

/mol_type="unassigned DNA"

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ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0

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Db 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGCAGCTGATCACCGCGGTC 261
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DEFINITION Sequence 351 from patent US 6426072.
ACCESSION AR220689
VERSION AR220689.1 GI:23327470
KEYWORDS
SOURCE
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REFERENCE
1 (bases 1 to 1012)
Wang, T., Fan, L., Kalos, M.D., Bangur, C.S., Hoeken, N.A., Fanger, G.R.,
Li, S.X., Wang, A., Skeiky, Y.A.W., Henderson, R.A., and McNeill, P.D.,
Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL
Patent: US 6426072-A 351 30-JUL-2002;
FEATURES
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AX369165
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FEATURES
ORIGIN
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Percent Similarity:
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Db 382 ACATTGGCGGAGGACCCCGGCC 405
RESULT 21
AR400556
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US-09-684-215B-18 (1-128) x AR400556 (1-1203)
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Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
Db 262 GACGGCGTCCGATCACTCGCCACACCGGATGGGACGCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyIleThrArgThrGlyAsnVal 120
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Unclassified.
1 (bases 1 to 1203)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 851 07-OCT-2003;
FEATURES Location/Qualifiers
source 1..1203
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 4,38e-44 Length: 1203
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
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QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyValAlaArgVal 60
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QY 121 ThrLeuAlaGluGlyProProAla 128
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RESULT 23
AX201078 1203 bp DNA linear PAT 29-AUG-2001
LOCUS
DEFINITION Sequence 708 from Patent WO0151633.
ACCESSION AX201078
VERSION AX201078.1 GI:15390883
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 708 19-JUL-2001;
FEATURES CORIXA CORPORATION (US)
Location/Qualifiers

source 1..1203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 4,38e-44 Length: 1203
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-19 (1-128) x AX201078 (1-1203)
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Db 22 ACGGCGCGTCCGATAAATTCAGCTGCCAGGGTGGCGAGGATTCCCGATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyValAlaArgVal 60
Db 142 GCCTTCTCGGCTTGGTGTTCGACACACACGCGACGCGGACGAGTCCACCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGGCGCTCCGCGCGAAGTCTCGCACTCCACCGGCGAGTGTATCAACCGGCTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCGACCGCGATGCGCGAGCGGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGGTACAGGAAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 24
AX267877 1203 bp DNA linear PAT 26-OCT-2001
LOCUS
DEFINITION Sequence 851 from Patent WO0173032.
ACCESSION AX267877
VERSION AX267877.1 GI:16516515
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 851 04-OCT-2001;
FEATURES CORIXA CORPORATION (US)
Location/Qualifiers
source 1..1203
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 4,38e-44 Length: 1203

Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX267877 (1-1203)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGGCTCCGATTAATTCAGCTGCCAGAGTGGGAGGATTCGCATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlnGlyValAlaArgValGlnArgVal 60
DB 142 GCCTTCTCGGCTTGGGTGTGTGCACAAACGCAACGCGGACGAGTCCAAAGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACGGCGAGTGCATCACCGCGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGCGCTCCGATCAACTCCGCCACCGGATGGCGGACGCGCTTAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTATCTCGTGACCTGGCAACCAAGTCCGGCGGACGCGTACAGGAAACGTG 381
QY 121 ThrLeuAlaGluGlyProProIle 128
DB 382 ACATTGGCGAGGACCCCGGCC 405

RESULT 25

LOCUS AR229410 1464 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 348 from patent US 6448234.
ACCESSION AR229410
VERSION AR229410.1 GI:27268663
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Alignment Scores:
Pred. No.: 5,37e-44 Length: 1464
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR229410 (1-1464)

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QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40

DB 82 GGGCAGGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGCTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlnGlyValAlaArgValGlnArgVal 60
DB 142 GCCTTCTCGGCTTGGGTGTGTGCACAAACGCAACGCGGACGAGTCCAAAGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACGGCGAGTGCATCACCGCGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGCGCTCCGATCAACTCCGCCACCGGATGGCGGACGCGCTTAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTATCTCGTGACCTGGCAACCAAGTCCGGCGGACGCGTACAGGAAACGTG 381
QY 121 ThrLeuAlaGluGlyProProIle 128
DB 382 ACATTGGCGAGGACCCCGGCC 405

RESULT 26

LOCUS AR322028 1464 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 348 from patent US 6565856.
ACCESSION AR322028
VERSION AR322028.1 GI:33707372
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Alignment Scores:
Pred. No.: 5,37e-44 Length: 1464
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AR322028 (1-1464)

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QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGCTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlnGlyValAlaArgValGlnArgVal 60
DB 142 GCCTTCTCGGCTTGGGTGTGTGCACAAACGCAACGCGGACGAGTCCAAAGCGGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACGGCGAGTGCATCACCGCGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGCGCTCCGATCAACTCCGCCACCGGATGGCGGACGCGCTTAACGGGATCATCCC 321

Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGCGGCACGGGTACAGGAAACGTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGACCCCGGCC 405

RESULT 27
AX156105
LOCUS AX156105 1464 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 348 from Patent WO0140474.
ACCESSION AX156105
VERSION AX156105.1 GI:14537130
KEYWORDS Chlamydia trachomatis
SOURCE Chlamydia trachomatis
ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE 1
AUTHORS Probst, P., Bhatia, A., Skeiky, Y.A., Fling, S.P. and Scholler, J.
TITLE Compounds and methods for treatment and diagnosis of chlamydial infection
JOURNAL Patent: WO 0140474-A 348 07-JUN-2001;
CORIXA CORPORATION (US)
FEATURES
source 1. .1464
/organism="Chlamydia trachomatis"
/mol_type="unassigned DNA"
/db_xref="taxon:813"

ORIGIN
Alignment Scores:
Pred. No.: 5,37e-44 Length: 1464
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX156105 (1-1464)

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Db 22 ACGCGCGCTCCGATTAATCTCCAGCTGTCACAGGTGGCGAGGATTCGGCATTCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTTGGGTGTGTCGACAAACACGCGACGCGGACGAGTCCACGCGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGCGATCACCAGCGGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
Db 262 GACGCGCTCCGATCAACTCGGCCACCGCATGGCGGACGCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGCGGCACGGGTACAGGAAACGTG 381

RESULT 28
AX361955
LOCUS AX361955 1464 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 348 from Patent WO0208267.

ACCESSION AX361955
VERSION AX361955.1 GI:18694417
KEYWORDS Chlamydia trachomatis
SOURCE Chlamydia trachomatis
ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

REFERENCE 1
AUTHORS Fling, S.P., Skeiky, Y.A., Probst, P. and Bhatia, A.
TITLE Compounds and methods for treatment and diagnosis of chlamydial infection
JOURNAL Patent: WO 0208267-A 348 31-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source 1. .1464
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/mol_type="unassigned DNA"
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-18 (1-128) x AX361955 (1-1464)

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGCGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTTGGGTGTGTCGACAAACACGCGACGCGGACGAGTCCACGCGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGCGATCACCAGCGGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
Db 262 GACGCGCTCCGATCAACTCGGCCACCGCATGGCGGACGCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGCGGCACGGGTACAGGAAACGTG 381

RESULT 29
AX229398
LOCUS AX229398 1557 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 332 from patent US 6448234.
ACCESSION AR229398
VERSION AR229398.1 GI:27268651
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1557)
AUTHORS Fling, S.P.
TITLE Compounds and methods for treatment and diagnosis of chlamydial infection
JOURNAL Patent: US 6448234-A 332 10-SEP-2002;
FEATURES Location/Qualifiers

Qy	1	ThrAlaSerAspAsn	PheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIle	Profile	20
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Qy	21	GlyGlnAlaMetAlaIle	AlaGlyGlnIleLysLeuProThrValHisIleGlyProThr		40
Db	82	GGCAGCGCATGGCGAT	TCGGGGCCAGATCAAGCTCCACCGTTTCATATCGGGCTACC		141
Qy	41	AlaPheLeuGlyLeuGlyValVal	AspAsnAsnGlyAsnGlyAlaArgValGlnArgVal		60
Db	142	GCTTCTTCGGCTGGGTGT	GTGCGACACACGGGACGGCGACAGTCCACGGCTG		201
Qy	61	ValGlySerAlaProAlaAlaSer	LeuGlyIleSerThrGlyAspValIleThrAlaVal		80
Db	202	GTCGGGACGCTCCGGCGGCA	GCTCGGCATCTCCACCGGGACGTATCACCGGGTC		261
Qy	81	AspGlyAlaProfileAsnSerAla	ThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro		100
Db	262	GACGGCGCTCCGATCACT	CGGCGCACCGCGATGGCGGACGCGCTTACCGGCATCATCCC		321
Qy	101	GlyAspValIleSerValThrTrp	GlnThrLysSerGlyGlyThrArgThrGlyAsnVal		120
Db	322	GGTGACGTCATCTCGGTGAC	CTCGCAACCCAAAGTCGGGGCGCACCGGTACGGGAACGTTG		381
Qy	121	ThrLeuAlaGluGlyProProAla		128	
Db	382	ACATGGCCGAGGAC	CCCCCGGCC	405	

Search completed: April 30, 2004, 02:24:05
Job time : 3674.05 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 20:30:12 ; Search time 364.096 Seconds
(without alignments)
1493.479 Million cell updates/sec

Title: US-09-684-215B-23
Perfect score: 651
Sequence: 1 TAAADNFQLSQGGQGAIP1.....SVTQTKSGTGTGNVTLAE 128

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	100.0	396	4 AAL40769	Aal40769 Nucleotid
2	651	100.0	672	4 AAL40772	Aal40772 Nucleotid
3	651	100.0	702	2 AAZ20206	Aaz20206 Mycobacte
4	651	100.0	702	4 AAL40770	Aal40770 Nucleotid
5	651	100.0	702	6 ABK14140	Abk14140 DNA encod
6	651	100.0	1002	6 AAD47078	Aad47078 Mycobacte
7	651	100.0	1002	6 AAD47077	Aad47077 Mycobacte
8	651	100.0	1002	6 AAD28336	Aad28336 Mycobacte

9	651	100.0	1002	6 AAD28337	Aad28337 Mycobacte
10	651	100.0	1068	2 AAX34251	Aax34251 Mycobacte
11	651	100.0	1143	2 AAX34252	Aax34252 Mycobacte
12	651	100.0	1629	5 AAS03793	Aas03793 M. tuberc
13	651	100.0	1742	4 AAL40771	Aal40771 Nucleotid
14	651	100.0	1871	4 AAL40768	Aal40768 Nucleotid
15	651	100.0	2181	8 ADA26353	Ada26353 Mycobacte
16	651	100.0	2190	6 AAD47084	Aad47084 Mycobacte
17	651	100.0	2190	6 AAD28343	Aad28343 Mycobacte
18	651	100.0	2191	4 AAL40773	Aal40773 Nucleotid
19	651	100.0	2286	6 ABK14128	Abk14128 DNA encod
20	651	100.0	2287	2 AAZ20194	Aaz20194 Mycobacte
21	651	100.0	2287	6 AAD47083	Aad47083 Mycobacte
22	651	100.0	2287	6 AAD28342	Aad28342 Mycobacte
23	651	100.0	2451	8 ADA26360	Ada26360 Mycobacte
24	651	100.0	2487	8 ADA26359	Ada26359 Mycobacte
25	651	100.0	2637	8 ADA28358	Ada28358 Mycobacte
26	651	100.0	2808	6 AAD47110	Aad47110 Mycobacte
27	651	100.0	2808	8 ADA26357	Ada26357 Mycobacte
28	651	100.0	3030	8 ADA26355	Ada26355 Mycobacte
29	651	100.0	3060	8 ADA26363	Ada26363 M. bovis
30	651	100.0	3104	8 ADA26362	Ada26362 Mycobacte
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34	646	99.2	447	2 AAT91403	Aat91403 Mycobacte
35	646	99.2	447	2 AAT91466	Aat91466 Mycobacte
36	646	99.2	447	2 AAV44342	Aav44342 Mycobacte
37	646	99.2	447	2 AAV64450	Aav64450 M. tuberc
38	646	99.2	447	2 AAZ19040	Aaz19040 M. tuberc
39	646	99.2	447	2 AAZ19252	Aaz19252 M. tuberc
40	646	99.2	447	5 AAS03780	Aas03780 M. tuberc
41	646	99.2	447	6 AAD47080	Aad47080 Mycobacte
42	646	99.2	447	6 AAD28339	Aad28339 Mycobacte
43	646	99.2	1872	2 AAT91414	Aat91414 Mycobacte
44	646	99.2	1872	2 AAT91477	Aat91477 Mycobacte
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ALIGNMENTS

RESULT 1

AAL40769
ID AAL40769 standard; DNA; 396 BP.

XX AAL40769;

XX AC AAL40769;

XX DT 03-OCT-2002 (first entry)

XX DE Nucleotide sequence encoding Ral2 protein.

XX KW Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;

XX KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;

XX KW immunogen; cytokine; gene; ds.

XX OS Unidentified.

XX PH Location/Qualifiers

XX FT CDS

XX FT 1..396

XX FT /*tag= a

XX FT /product= "Ral2 protein"

XX FT /note= "No start or stop codon"

XX PN WO200125401-A2.

XX PD 12-APR-2001.

XX PF 06-OCT-2000; 2000WO-US027652.

XX PR 07-OCT-1999; 99US-0158585P.

XX PA (CORI-) CORIXA CORP.

PI Skeiky Y, Guderian J;
 XX WPI; 2001-266299/27.
 DR P-PSDB; AAO22138.
 XX
 XX Recombinant nucleic acid molecule for producing high yield expression of
 PT desired fusion polypeptides, encodes fusion polypeptide comprising
 PT Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
 XX
 XX Claim 1; Fig 2; 39pp; English.
 PS
 XX The invention relates to a recombinant nucleic acid molecule encoding a
 CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
 CC kDa C-terminal fragment of serine protease antigen Mtb32A of
 CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
 CC The recombinant fusion nucleic acids and polypeptides are useful for
 CC providing stable and high yield expression of fusion polypeptides of both
 CC eukaryotic and prokaryotic origin and to encode a protein product for use
 CC as an antigen for detecting serum antibodies. The presence of serum
 CC antibodies to M. tuberculosis antigens in an individual indicates that
 CC the individual is infected with it. The fusion polypeptides are useful as
 CC sources of proteins for monitoring binding of serum antibodies to fusion
 CC proteins and as an immunogen to induce and/or enhance immune responses.
 CC The coding sequences can be ligated with a coding sequence of another
 CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
 CC can be used in vivo as a DNA vaccine. This polynucleotide sequence
 CC represents the DNA encoding the Ral2 protein
 XX
 XX Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 9,698-55 Length: 396
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps:

US-09-684-215B-23 (1-128) x AAL40769 (1-396)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 1 ACGGCGCGTCCGATTAATTCAGCTGCCAGGTGGCGAGGATTCGCCATTCGGATC 60
 QY 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlyGlySerProThrValHis 40
 DB 61 GGGCAGGCGATCGCATCGCGGCAGATCCGATCGGGTGGGGGTCCACCCCGTTTCAT 120
 QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
 DB 121 ATCGGCGCTACCGCTTCTCGGCTTGGTGTGTCGACACACACGCGACGCGACGA 180
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 181 GTCCACGCGTGTGCGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGGACGTG 240
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 DB 241 ATCACCAGCGGTGACCGGCGCTCCGATCACTCGGCCACCGCATGGCGGACGCGTTAAC 300
 QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyThrArg 120
 DB 301 GGGCATCATCCCGGTGACGTGATCTCGTGACCTGGCAAAACCAAGTCGGGCGGCGCGGT 360
 QY 121 ThrGlyAsnValThrLeuAlaGlu 128
 DB 361 ACAGGGAACGTGACATTTGCCGAG 384

RESULT 2
 AAL40772
 ID AAL40772 standard; DNA; 672 BP.
 XX
 XX AC AAL40772;

XX 06-AUG-2003 (revised)
 DT 03-OCT-2002 (first entry)
 XX
 XX Nucleotide sequence encoding Ral2-mammaglobin fusion protein.
 DE
 XX Ral2; serine protease antigen; Mtb32A; Mycobacterium tuberculosis;
 KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
 KW immunogen; cytokine; gene; ds.
 XX
 OS Mammalia.
 OS Unidentified.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT 4..666
 FT /*tag= a
 FT /product= "Ral2-mammaglobin fusion protein"
 XX
 PN W0200125401-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US027652.
 XX
 PF 07-OCT-1999; 99US-015858SP.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Skeiky Y, Guderian J;
 PI
 XX WPI; 2001-266299/27.
 DR P-PSDB; AAO22141.
 XX
 XX Recombinant nucleic acid molecule for producing high yield expression of
 PT desired fusion polypeptides, encodes fusion polypeptide comprising
 PT Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
 XX
 XX Disclosure; Fig 5; 39pp; English.
 PS
 XX The invention relates to a recombinant nucleic acid molecule encoding a
 CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
 CC kDa C-terminal fragment of serine protease antigen Mtb32A of
 CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
 CC The recombinant fusion nucleic acids and polypeptides are useful for
 CC providing stable and high yield expression of fusion polypeptides of both
 CC eukaryotic and prokaryotic origin and to encode a protein product for use
 CC as an antigen for detecting serum antibodies. The presence of serum
 CC antibodies to M. tuberculosis antigens in an individual indicates that
 CC the individual is infected with it. The fusion polypeptides are useful as
 CC sources of proteins for monitoring binding of serum antibodies to fusion
 CC proteins and as an immunogen to induce and/or enhance immune responses.
 CC The coding sequences can be ligated with a coding sequence of another
 CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
 CC can be used in vivo as a DNA vaccine. This polynucleotide sequence
 CC represents the DNA encoding the Ral2-mammaglobin fusion protein. (Updated
 CC on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 672 BP; 160 A; 195 C; 187 G; 140 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 1,798-54 Length: 672
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps:

US-09-684-215B-23 (1-128) x AAL40772 (1-672)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 25 ACGGCGCGTCCGATTAATTCAGCTGCCAGGTGGCGAGGATTCGCCATTCGGATC 84

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 85 GGGCAGCGGATGGCGATCGGGGCCAGATCGATCGGTTGGGGGTCAACCCACCGTTTCA 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
DB 145 ATCGGGCTACCGCTTCTCGGCTGGGTGTTGTCGACAAACGCGCAACGCGCGCAGCA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 205 GTCCACGCGTGGTCGGAGGCTCCGGCGCAGATCTCGGCATCTCCACCGCGCGCTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 265 ATCACCGCGTGGCGGCTCCGATCAACTCGGCCACCGCGATGGCGGCGGCTTAAC 324
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleValSerGlyGlyThrArg 120
DB 325 GGGCATATCCCGTGAGCTATCTCGTGACCTGGCAACCAAGTCGGCGGCGACCGCT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 385 ACAGGGAACGTGACATTGGCCGAG 408
RESULT 3
AAZ20206
ID AAZ20206 standard; DNA; 702 BP.
AC AAZ20206;
AT 17-JAN-2000 (first entry)
DE Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA.
XX Tuberculosis; antigen; fusion protein; Mtb24; Ra12; DPPD; diagnosis;
KW therapy; vaccine; immunogen; ss.
OS Mycobacterium tuberculosis.
XX WO9951748-A2.
FN 14-OCT-1999.
XX 07-APR-1999; 99WO-US007717.
XX 07-APR-1998; 98US-00056556.
PR 30-DEC-1998; 98US-00223040.
XX (CORI-) CORIXA CORP.
PA Skeiky YAW, Alderson M, Campos-Neto A;
PI WPI; 1999-601610/51.
XX P-PSDB; AAY32071.
XX New fusion proteins useful for diagnosis, prevention and treatment of
PT tuberculosis.
PS Example; Fig 13A-B; 83pp; English.
XX This DNA sequence includes a coding region for a recombinant
CC Mycobacterium tuberculosis bi-antigen fusion protein (see AAY32071),
CC termed Mtb24, composed of the antigens Ra12 and DPPD. The DNA is useful
CC for the recombinant production of the fusion protein. Coding sequences
CC for the antigens were modified by PCR in order to facilitate their fusion
CC and subsequent expression of the fusion protein, and then ligated. The
CC invention provides fusion proteins (see AAY32059-71) containing at least
CC 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides
CC encoding them are useful as vaccines for preventing tuberculosis
CC (claimed), for diagnosis (via in vitro assays or intradermal skin tests
CC for detection of anti-M. tuberculosis antibodies), monitoring of disease
CC progression, and treatment of tuberculosis. They are more effective

CC immunogens than mixtures of the individual protein components
XX Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 1.88e-54 Length: 702
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-684-215B-23 (1-128) x AAZ20206 (1-702)
QY 1 ThrAlaIleSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 25 ACGGCGCGGTCCGATAACTTCCAGCTGTCCAGGGTGGGCGAGGATTCCGCATTCCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 85 GGGCAGCGATGGCGATCGGGGCCAGATCGATCGGTTGGGGGTCAACCCACCGTTTCA 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
DB 145 ATCGGGCTACCGCTTCTCGGCTGGGTGTTGTCGACAAACGCGCAACGCGCGCAGCA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 205 GTCCACGCGTGGTCGGAGGCTCCGGCGCAGATCTCGGCATCTCCACCGCGCGCTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 265 ATCACCGCGTGGCGGCTCCGATCAACTCGGCCACCGCGATGGCGGCGGCTTAAC 324
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleValSerGlyGlyThrArg 120
DB 325 GGGCATATCCCGTGAGCTATCTCGTGACCTGGCAACCAAGTCGGCGGCGACCGCT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 385 ACAGGGAACGTGACATTGGCCGAG 408
RESULT 4
AAL40770
ID AAL40770 standard; DNA; 702 BP.
XX AAL40770;
AC AAL40770;
XX 03-OCT-2002 (first entry)
DE Nucleotide sequence encoding Ra12-DPPD fusion protein.
XX Ra12; serine protease antigen; Mtb32A; Mycobacterium tuberculosis;
KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
KW immunogen; cytokine; gene; ds.
XX Unidentified.
OS Chimeric.
XX Key Location/Qualifiers
FH 4. .896
FT CDS /tag= a
FT /product= "Ra12-DPPD fusion protein"
XX WO200125401-A2.
XX 12-APR-2001.
XX 06-OCT-2000; 2000WO-US027652.
XX 07-OCT-1999; 99US-0158585P.
XX (CORI-) CORIXA CORP.
PA

```
XX PI Skeiky Y, Guderian J;
XX DR WPI; 2001-266299/27.
XX DR P-PSDB; AAO22139.
XX XX
XX XX Recombinant nucleic acid molecule for producing high yield expression of
PT desired fusion polypeptides, encodes fusion polypeptide comprising
PT Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
XX PS
XX PS Example 1; Fig 3; 39pp; English.
XX CC
XX CC The invention relates to a recombinant nucleic acid molecule encoding a
CC fusion polypeptide, comprising a polynucleotide sequence of Ra12, a 14
CC kDa C-terminal fragment of serine protease antigen MTB32A of
CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
CC The recombinant fusion nucleic acids and polypeptides are useful for
CC providing stable and high yield expression of fusion polypeptides of both
CC eukaryotic and prokaryotic origin and to encode a protein product for use
CC as an antigen for detecting serum antibodies. The presence of serum
CC antibodies to M. tuberculosis antigens in an individual indicates that
CC the individual is infected with it. The fusion polypeptides are useful as
CC sources of proteins for monitoring binding of serum antibodies to fusion
CC proteins and as an immunogen to induce and/or enhance immune responses.
CC The coding sequences can be ligated with a coding sequence of another
CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
CC can be used in vivo as a DNA vaccine. This polynucleotide sequence
CC represents the DNA encoding the Ra12-DPPD fusion protein
XX SQ Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.88e-54 Length: 702
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x AAL40770 (1-702)
Qy 1 ThrAlaLaserAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGCCGGCTCCGATTAACCTTCACGTCTCCAGGGTGGCAGGATTCGGCATTCGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGCGGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTCCACCCACCGTTTCAT 144
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAenGlyValAlaArg 60
Db 145 ATCGGGCTACCGCTTCTCGGTTCGGTGTTCACACACACGCGACGCGGACGACGA 204
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGCGTGGTGGGAGGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCGATG 264
Qy 81 IleThrAlaValAspGlyValProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCAGGCTCGACGGCGCTCCGATCACTCGGCCACCGGATCGCGGACGCGCTTAC 324
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerglyGlyThrArg 120
Db 325 GGGCATCATCCGGTGACGTATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 384
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGAACGTCGACATGGCCGAG 408

RESULT 5
ABK14140
ID ABK14140 standard; DNA; 702 BP.
XX XX
```

```
AC ABK14140;
XX 29-AUG-2003 (revised)
DT 08-MAY-2002 (first entry)
XX XX
XX XX DNA encoding antigenic fusion protein Ra12-DPPD (Mtb24) .
XX XX Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
KW tuberculostatic; immunogen; vaccine; Ra12-DPPD; Mtb24.
XX XX
XX OS Mycobacterium tuberculosis.
OS Chimeric.
XX XX Location/Qualifiers
FT 1..702
CDS /tag= a
/product= "Mtb24 #1"
/partial
FT /transl_except= (pos:694..696, aa:Xaa)
FT /note= "No start or stop codon. Xaa= In frame stop codon"
CDS 2..702
/tag= b
/product= "Mtb24 #2"
/partial
FT /note= "No start or stop codon"
FT /transl_except= (pos:263..265, aa:Xaa) /transl_except=
(pos:353..355, aa:Xaa) /transl_except= (pos:395..397,
aa:Xaa) /transl_except= (pos:470..472, aa:Xaa)
FT /transl_except= (pos:701..702, aa:Ser)
FT /note= "This codon has an apparent 1 nucleotide deletion
which alters the reading frame. Xaa= In frame stop codon"
CDS 3..701
/tag= c
/product= "Mtb24 #3"
/partial
FT /note= "No start or stop codon"
FT /transl_except= (pos:1..2, aa:Pro) /transl_except=
(pos:339..341, aa:Xaa) /transl_except= (pos:321..323,
aa:Xaa) /transl_except= (pos:339..341, aa:Xaa)
FT /transl_except= (pos:450..452, aa:Xaa) /transl_except=
(pos:621..623, aa:Xaa)
FT /note= "No start or stop codon. Xaa= In frame stop codon"
XX XX
XX XX US2002009459-A1.
XX 24-JAN-2002.
XX 07-APR-1999; 99US-00287849.
XX 13-MAR-1997; 97US-00818112.
XX 01-OCT-1997; 97US-00942578.
XX 18-FEB-1998; 98US-00025197.
XX 07-APR-1998; 98US-00056556.
XX 30-DEC-1998; 98US-00223040.
XX (REED/) REED S G.
PA (SKEI/) SKEIKY Y A.
PA (DILL/) DILLON D C.
PA (ALDE/) ALDERSON M.
PA (CAMF/) CAMPOS-NETO A.
XX XX
XX PI Reed SG, Skeiky YA, Dillon DC, Alderson M, Campos-Neto A;
XX XX WPI; 2002-171134/22.
XX P-PSDB; AAU74600, AAU76541, AAU76542.
XX XX
XX XX New fusion proteins of Mycobacterium tuberculosis antigens, useful for
PT diagnosing, treating or preventing M. tuberculosis infection,
PT particularly as vaccine for treating or preventing tuberculosis.
XX XX
XX XX Example; Fig 13; 62pp; English.
XX XX
XX XX The invention relates to a purified polypeptide which induces an immune
```

CC response of Mycobacterium tuberculosis. Polypeptides of the invention are
CC useful for diagnosing, treating or preventing M. tuberculosis infection,
CC particularly tuberculosis infection. In particular, the polypeptides are
CC useful as a vaccine formulation with an adjuvant to afford long-term
CC protection in animals against the development of tuberculosis. The
CC protein coding sequence may be used to encode a protein product for use
CC as an immunogen to induce and/or enhance an immune response to M.
CC tuberculosis. This sequence represents DNA encoding an M. tuberculosis
CC fusion protein of the invention. This polynucleotide encodes 3 different
CC proteins, each in a different reading frame. (Updated on 29-AUG-2003 to
CC standardise OS field)

XX SQ Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.88e-54 Length: 702
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-23 (1-128) x ABK14140 (1-702)

Qy 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 25 ACGCCCGCTCCGATTAATCTCCAGCTGTCCAGGGTGGGAGGGATTGCCATTCGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTCCACCACCGTTTCAT 144
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAenGlyAenGlyAlaArg 60
Db 145 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTCGACCAACAGCGGACGGCGACGA 204
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCACACGGCTGCTGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 264
Qy 81 IleThrAlaValAlaGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCAGCGTGCAGCGCTCCGATCACTCGGCCACCGGATGGCGGACGGCTTAAC 324
Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 325 GGGCATCATCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTGGGGCGGACGCGT 384
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 6
ID AAD47078
ID AAD47078 standard; DNA; 1002 BP.
XX AAD47078;
AC AAD47078;
XX 27-JAN-2003 (first entry)
DE Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein DNA.
XX Vaccine; immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant;
KW gene; antigen; ds.
XX Mycobacterium tuberculosis.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 4..996
FT /*tag= a
FT /product= "Ra35FLMutSA mutant antigenic protein"
XX

FN WO200272792-A2.
XX 19-SEP-2002.
XX 13-MAR-2002; 2002WO-US008223.
XX 13-MAR-2001; 2001US-0275837P.
XX (CORI-) CORIXA CORP.
PI Skeiky Y, Brannon M, Guderian J;
DR WPI: 2002-759844/82.
DR P-PSDB; AAE29703.
XX New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,
PT M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
PT against pathogenic microorganisms e.g. Leishmania and Mycobacterium
PS tuberculosis.
XX Disclosure; Page 80-81; 155pp; English.

CC The invention relates to a recombinant nucleic acid molecule encoding a
CC fusion polypeptide. The recombinant nucleic acid comprises a heterologous
CC polynucleotide sequence encoding an antigen or an antigenic fragment from
CC Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
CC polypeptide or its fragment. The Leishmania polynucleotide is selected
CC from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention
CC are used in methods for eliciting immune response in mammals. They are
CC useful as vaccines to elicit protective immunity against pathogenic
CC microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
CC polypeptides are used for enhancing the expression of polynucleotides, as
CC in vivo diagnostic agents and for raising antibodies in a non-human
CC animal. The invention is used in gene therapy. The present sequence is M.
CC tuberculosis Ra35FLMutSA mutant antigenic protein encoding DNA

SQ Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.85e-54 Length: 1002
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-23 (1-128) x AAD47078 (1-1002)

Qy 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 598 ACGCCCGCTCCGATTAATCTCCAGCTGTCCAGGGTGGGAGGGATTGCCATTCGATC 657
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 658 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTCCACCCACCGTTTCAT 717
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAenGlyAenGlyAlaArg 60
Db 718 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTCGACCAACAGCGGACGGCGACGA 777
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 778 GTCCACACGGCTGCTGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGCGT 837
Qy 81 IleThrAlaValAlaGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 838 ATCACCAGCGTGCAGCGCTCCGATCACTCGGCCACCGGATGGCGGACGGCTTAAC 897
Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 898 GGGCATCATCCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTGGGGCGGACGCGT 957
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

```
Db 958 ACAGGGAACGTGACATTGGCCGAG 981
|||||
RESULT 7
AAD47077
ID AAD47077 standard; DNA; 1002 BP.
XX
AC AAD47077;
XX
DT 27-JAN-2003 (first entry)
XX
DE Mycobacterium tuberculosis mature Ra35 antigen encoding DNA.
XX
XX Vaccine; immunity; diagnostic agent; gene therapy; Ra35 antigen; gene;
KW ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT CDS 4..996
FT /product= "Ra35 mature antigenic protein"
FT /transl_except= (pos:547..549, aa:Asp)
FT /transl_except= (pos:550..552, aa:Ser)
XX
XX WO200272792-A2.
XX
XX 19-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-US008223.
XX
XX 13-MAR-2001; 2001US-0275837P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Brannon M, Guderian J;
XX
XX WPI; 2002-759844/82.
XX
XX P-PSDB; AAE29702.
XX
XX New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,
XX M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
XX against pathogenic microorganisms e.g. Leishmania and Mycobacterium
XX tuberculosis.
XX
XX Disclosure; Page 79; 155pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
XX fusion polypeptide. The recombinant nucleic acid comprises a heterologous
XX polynucleotide sequence encoding an antigen or an antigenic fragment from
XX Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
XX polypeptide or its fragment. The Leishmania polynucleotide is selected
XX from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention
XX are used in methods for eliciting immune response in mammals. They are
XX useful as vaccines to elicit protective immunity against pathogenic
XX microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
XX polypeptides are used for enhancing the expression of polynucleotides, as
XX in vivo diagnostic agents and for raising antibodies in a non-human
XX animal. The invention is used in gene therapy. The present sequence is M.
XX tuberculosis mature Ra35 (N-terminus of MTB32A; RA35FL) antigen encoding
XX DNA
XX
XX Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,85e-54 Length: 1002
XX Score: 651.00 Matches: 128
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-684-215B-23 (1-128) x AAD47077 (1-1002)
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```
QY 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlyGlnGlyGlyPheAlaIleProIle 20
Db 598 ACAGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCAGGAGATTCCGCATTCOGATC 657
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 658 GGGCAGCGGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTACCCACCGTTTCAT 717
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAenAenGlyAsnGlyAlaArg 60
Db 718 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTTCGACACAAACACGCAACGGGCGACGA 777
QY 61 ValGlnArgValValGlySerAlaPheAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 778 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGGGACGTG 837
QY 81 IleThrAlaValAspGlyValAlaProIleAenSerAlaThrAlaMetAlaAspAlaLeuAen 100
Db 838 ATCACCGCGTCCGCGCGCTCCGATCAATCAATCGGCGCACCGCGATGGCGGCGCTTAAC 897
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 898 GGGCATCATCCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGGCGGCGGT 957
QY 121 ThrGlyAenValThrLeuAlaGlu 128
Db 958 ACAGGGAACGTGACATTGGCCGAG 981
RESULT 8
AAD28336
ID AAD28336 standard; cDNA; 1002 BP.
XX
AC AAD28336;
XX
DT 22-APR-2002 (first entry)
XX
DE Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding cDNA.
XX
XX Fusion protein; antigen; serological sensitivity; immune response;
XX tuberculosis; infection; vaccine; MTB32A; Ra32FL; ss.
XX
XX Mycobacterium sp.
XX
XX Key Location/Qualifiers
XX FH 4..996
XX CDS /tag= a
XX /product= "Ra35 mature protein"
XX /transl_except= (pos:547..549, aa:Asp)
XX /transl_except= (pos:550..552, aa:Ser)
XX
XX WO200198460-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019959.
XX
XX 20-JUN-2000; 2000US-00597796.
XX
XX 01-FEB-2001; 2001US-0265737P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Reed S, Alderson M;
XX
XX WPI; 2002-147798/19.
XX
XX P-PSDB; AAE17566.
XX
XX Composition comprising MTB39 antigen and MTB2A antigen from
XX Mycobacterium species, useful for eliciting immune response in a subject.
XX
XX Disclosure; Page 95; 136pp; English.
XX
XX The present invention relates to fusion proteins containing at least two
```


CC Mycobacterium species antigens, nucleotides encoding them and
CC compositions comprising such fusion proteins. The present invention
CC particularly relates to nucleic acids encoding fusion proteins that
CC include two or more individual M. tuberculosis antigens which increase
CC the serological sensitivity of sera from individuals infected with
CC tuberculosis and methods for their use in diagnosis, prevention and
CC treatment of tuberculosis infection. Sequences of the invention are
CC useful for eliciting an immune response in a mammal, e.g., human,
CC immunised with BCG. They are useful in the diagnosis, treatment and
CC prevention of Mycobacterium infection. The fusion proteins and the
CC polynucleotides are useful as diagnostic tools in patients infected with
CC Mycobacterium, in vitro and in vivo assays for detecting humoral
CC antibodies or cell-mediated immunity against M. tuberculosis, for the
CC diagnosis of an infection or monitoring of disease progression, as
CC immunogens to generate or elicit a protective immune response in a
CC patient and for raising anti-M. tuberculosis antibodies in a non-human
CC animal. Sequences of the invention are also used as vaccines. MTB32A
CC fusion proteins of the invention are useful as in vivo diagnostic agents
CC for intradermal skin test. The present sequence is a cDNA encoding
CC Mycobacterium species MTB32A (Ra32FL) mature protein
XX Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 2.85e-54 Length: 1002
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-684-215B-23 (1-128) x AAD28336 (1-1002)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
DB 598 ACGGCGCGGTCCGATTAATTCAGGTGCCAGGGTGGCGAGGATTCGCCATTCGCATC 657

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 658 GGGCAGCGCATGGCGATCCGGCGCCAGATCCGATCGGTGGGGGTACCCACCGTTTCAT 717

QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValAlaArg 60
DB 718 ATCGGGCTTACCGCTTCTCGGTGGTGGTGTTCGACACACGCGCAACGGCGCAGCA 777

QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 778 GTCCAAAGCGGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGCAGGTG 837

QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAlaLeuAsn 100
DB 838 ATCACCAGCGGTGCGAGCGGCTCCGATCACTCGGCACCGCATGGCGAGCGCGTTAAC 897

QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 898 GGGCATCATCCGGTGACGTATCTCGGTGACCTGGCAACCAAGTCCGGCGGCGCAGCGGT 957

QY 121 ThrGlyAsnValThrLeuAlaGln 128
DB 958 ACAGGGAGCGTGACATGGCCGAG 981

RESULT 9
AAD28337
ID AAD28337 standard; cDNA; 1002 BP.
XX
AC AAD28337;
XX
DT 22-APR-2002 (first entry)
XX
DE Mycobacterium species Ra35FLMutSA mutant cDNA.
KW Fusion protein; antigen; serological sensitivity; immune response;
KW tuberculosis; infection; vaccine; Ra32FLMutSA; mutant; mutetin; ss.

XX Mycobacterium sp.
OS
XX Key Location/Qualifiers
FH 4..996
FT CDS /*tag= a
FT /product= "Ra35FLMutSA protein"
XX
PN WO200198460-A2.
XX
XX 27-DEC-2001.
PD
XX 20-JUN-2001; 2001WO-US019959.
PF
XX 20-JUN-2000; 2000US-00597796.
PR 01-FEB-2001; 2001US-0265737P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Skeiky Y, Reed S, Alderson M;
PI WPI; 2002-147798/19.
XX P-PSDB; AAE17567.
DR
DR Composition comprising MTB39 antigen and MTB32A antigen from
PT Mycobacterium species, useful for eliciting immune response in a subject.
XX
XX Claim 67; Page 96-97; 136pp; English.
XX
CC The present invention relates to fusion proteins containing at least two
CC Mycobacterium species antigens, nucleotides encoding them and
CC compositions comprising such fusion proteins. The present invention
CC particularly relates to nucleic acids encoding fusion proteins that
CC include two or more individual M. tuberculosis antigens which increase
CC the serological sensitivity of sera from individuals infected with
CC tuberculosis and methods for their use in diagnosis, prevention and
CC treatment of tuberculosis infection. Sequences of the invention are
CC useful for eliciting an immune response in a mammal, e.g., human,
CC immunised with BCG. They are useful in the diagnosis, treatment and
CC prevention of Mycobacterium infection. The fusion proteins and the
CC polynucleotides are useful as diagnostic tools in patients infected with
CC Mycobacterium, in vitro and in vivo assays for detecting humoral
CC antibodies or cell-mediated immunity against M. tuberculosis, for the
CC diagnosis of an infection or monitoring of disease progression, as
CC immunogens to generate or elicit a protective immune response in a
CC patient and for raising anti-M. tuberculosis antibodies in a non-human
CC animal. Sequences of the invention are also used as vaccines. MTB32A
CC fusion proteins of the invention are useful as in vivo diagnostic agents
CC for intradermal skin test. The present sequence is a cDNA encoding
CC Mycobacterium species Ra32FL mature protein mutant, Ra32FLMutSA
XX Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 2.85e-54 Length: 1002
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-684-215B-23 (1-128) x AAD28337 (1-1002)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
DB 598 ACGGCGCGGTCCGATTAATTCAGGTGCCAGGGTGGCGAGGATTCGCCATTCGCATC 657

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 658 GGGCAGCGCATGGCGATCCGGCGCCAGATCCGATCGGTGGGGGTACCCACCGTTTCAT 717

QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValAlaArg 60
DB 718 ATCGGGCTTACCGCTTCTCGGTGGTGGTGTTCGACACACGCGCAACGGCGCAGCA 777

```

DB      718 ATCGGGCTACCGCTTCTCGGTGGTGTTCGCAACAACGCGAACGCGCGACGA 777
QY      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB      778 GTCCAAACGGTGTTCGGGAGCGCTCCGCGCGCAAGTCTCCGCATCTCCACCGCGACGTG 837
QY      81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB      838 ATCACCGCGGTGACGCGGCTCCGATCAACTCGGCCACCGCATGCGGAGCGCGCTTAAC 897
QY      101 GlyHisHisProGlyAspValIleSerValThrTTPGlnThrLysSerGlyGlyThrArg 120
DB      898 GGGCATCATCCCGGTGAGTCACTCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 957
QY      121 ThrGlyAsnValThrLeuAlaGlu 128
DB      958 ACAGGGAACGTGACATTGCGCGAG 981

RESULT 10
AAAX34251
ID      AAX34251 standard; DNA; 1068 BP.
XX
AC      AAX34251;
XX
DT      06-JUL-1999 (first entry)
XX
DE      Mycobacterium species nucleic acid sequence 50D.
XX
KW      Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW      hybridisation; detection; vaccine; immunisation; infection; ss.
XX
OS      Mycobacterium sp.
XX
PN      WO9909186-A2.
XX
PD      25-FEB-1999.
XX
PF      14-AUG-1998; 98WO-FR001813.
XX
PR      14-AUG-1997; 97FR-00010404.
XX
PR      11-SEP-1997; 97FR-00011325.
XX
PA      (INSP ) INST PASTEUR.
XX
PI      Gicquel B, Portnoie D, Lim E, Pellicic V, Guigueno A;
PI      Goguet De La Salmoniere Y;
XX
DR      WPI; 1999-181045/15.
DR      P-PSDB; AAY05000.
XX
PT      Mycobacterial DNA vectors containing reporter constructs - for
PT      identifying coding or promoter sequences involved in infection-associated
PT      protein expression.
XX
PS      Claim 22; Fig 50D; 309pp; French.
XX
CC      Sequences AAX34001-X34252 represent nucleic acids encoding secreted
CC      proteins from various Mycobacterium species microorganisms. The
CC      nucleotide sequences can be used as primers and probes for methods for
CC      detecting and identifying mycobacteria, especially belonging to the M.
CC      tuberculosis complex. The encoded proteins can be used in vaccines for
CC      immunisation against a bacterial or viral infection
XX
SQ      Sequence 1068 BP; 169 A; 352 C; 375 G; 172 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      3.06e-54      Length:      1068
Score:          651.00      Matches:      128
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:             2           Gaps:      0

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US-09-684-215B-23 (1-128) x AAX34251 (1-1068)
QY      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB      670 ACGGCGCGCTCCGATAACTTCCAGCTGTCCAGAGGTGGCGAGGATTGCCCATTCGGATC 729
QY      21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB      730 GGGCAGCGCATGGCGATCGCGGCGCATCCGATCGGTGGGGGTTCACCCACCGTTTCA 789
QY      41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
DB      790 ATCGGCGCTTACCGCTTCTCGGCTTGGGTGTTCGACCAACAACGCGCAACGCGCACGA 849
QY      61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB      850 GTCCAAACGGTGTTCGGGAGCGCTCGGCGCGCAAGTCTCGGCATCTCCACCGCGCGACGTG 909
QY      81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB      910 ATCACCGCGGTGACGCGCTCCGATCAACTCGGCCACCGCATGCGGAGCGCGCTTAAC 969
QY      101 GlyHisHisProGlyAspValIleSerValThrTTPGlnThrLysSerGlyGlyThrArg 120
DB      970 GGGCATCATCCCGGTGAGTCACTCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 1029
QY      121 ThrGlyAsnValThrLeuAlaGlu 128
DB      1030 ACAGGGAACGTGACATTGCGCGAG 1053

RESULT 11
AAAX34252
ID      AAX34252 standard; DNA; 1143 BP.
XX
AC      AAX34252;
XX
DT      06-JUL-1999 (first entry)
XX
DE      Mycobacterium species nucleic acid sequence 50F.
XX
KW      Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW      hybridisation; detection; vaccine; immunisation; infection; ss.
XX
OS      Mycobacterium sp.
XX
PN      WO9909186-A2.
XX
PD      25-FEB-1999.
XX
PF      14-AUG-1998; 98WO-FR001813.
XX
PR      14-AUG-1997; 97FR-00010404.
PR      11-SEP-1997; 97FR-00011325.
XX
PA      (INSP ) INST PASTEUR.
XX
PI      Gicquel B, Portnoie D, Lim E, Pellicic V, Guigueno A;
PI      Goguet De La Salmoniere Y;
XX
DR      WPI; 1999-181045/15.
DR      P-PSDB; AAY04830.
XX
PT      Mycobacterial DNA vectors containing reporter constructs - for
PT      identifying coding or promoter sequences involved in infection-associated
PT      protein expression.
XX
PS      Claim 22; Fig 50F; 309pp; French.
XX
CC      Sequences AAX34001-X34252 represent nucleic acids encoding secreted
CC      proteins from various Mycobacterium species microorganisms. The
CC      nucleotide sequences can be used as primers and probes for methods for
CC      detecting and identifying mycobacteria, especially belonging to the M.
CC      tuberculosis complex. The encoded proteins can be used in vaccines for

```

```
CC immunisation against a bacterial or viral infection
XX SQ Sequence 1143 BP; 189 A; 373 C; 395 G; 186 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3 31e-54 Length: 1143
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-684-215B-23 (1-128) x AAX34252 (1-1143)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 745 ACGGCGCGTCCGATTAACCTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGATC 804
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 805 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGTGGGGGTCAACCACCGTTTCAT 864
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 865 ATCGGGCTTACCGCTTCCCTGGCTTGGGTGTGTGACAAACGCAACGCGCACGA 924
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 925 GTCCACGCGTGTGCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGACGTG 984
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 985 ATCACCGCGTGCAGCGCTCCGATCACTCGGCCACCGCATGCGGACGCGCTTAAC 1044
QY 101 GlyHisHisProGlyAspValIleSerValThrTyrGlnThrIleValThrArg 120
Db 1045 GGGCATCATCCGCTGAGCTCATCTCGTGCACCTGGCAACCAAGTCGGCGCGACGCT 1104
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 1105 ACAGGAACGTGACATGGCCGAG 1128

RESULT 12
AAS03793
ID AAS03793 standard; DNA; 1629 BP.
XX AC AAS03793;
XX DT 29-AUG-2001 (first entry)
XX DE M. tuberculosis DNA encoding antigen HTCC#1 fusion protein #4.
XX KW TBRAl2-HTCC#1; antigen; vaccine; tuberculosis; AIDS;
XX KW acquired immunodeficiency disease; His Tag; ds.
XX OS Mycobacterium tuberculosis.
XX FH Location/Qualifiers
XX CDS 1..1629
XX FT /*tag= a
XX FT /product= "TBRAl2-HTCC#1"
XX FT /transl_except= {pos:1621..1623,aa:Xaa}
XX FT /note= "Xaa= In frame STOP codon"
XX FT /partial
XX FT /note= "No start or stop codon. Although the sequence
XX FT does contain an in frame stop codon, 2 further amino
XX FT acids are shown in Figure 8 as being encoded by the
XX FT present sequence, without a further stop codon"
XX FT 25..426
XX FT misc_feature
XX FT /*tag= b
XX FT /note= "Region derived from TBRAl2"
XX FT 427..444
XX FT misc_feature
```

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FT FT /*tag= c
FT FT /note= "Region derived from Thrombin"
FT FT 445..1629
FT FT d
FT FT /*tag=
FT FT /note= "Region derived from HTCC#1"

WO200124820-A1.
12-APR-2001.
10-OCT-2000; 2000WO-US028095.
07-OCT-1999; 99US-0158338P.
07-OCT-1999; 99US-0158425P.
(CORI-) CORIXA CORP.
Skeiky Y, Reed S, Houghton RL, Mcneill PD, Dillon DC, Lodes ML;
WPI; 2001-290576/30.
Vaccinating against Mycobacteria infections in mammals using fusion
proteins comprising combinations of heterologous antigens.
Example 2; Fig 8; 168pp; English.
The sequence encodes Mycobacterium tuberculosis fusion protein, TBRAl2-
HTCC#1 and includes a His tag at the N-terminus to aid purification.
Compositions comprising at least 2 heterologous antigens, as a fusion
protein, and vectors expressing the fusion proteins are used as vaccines
to prophylactically immunise mammals (especially humans) against
infection by Mycobacteria. The compositions contain at least 2
heterologous antigens that increase the serological sensitivity of
CC individuals infected with tuberculosis, a disease frequently affecting
patients with acquired immunodeficiency disease, AIDS
SQ Sequence 1629 BP; 298 A; 500 C; 535 G; 296 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5e-54 Length: 1629
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-684-215B-23 (1-128) x AAS03793 (1-1629)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATTAACCTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 85 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGTGGGGGTCAACCACCGTTTCAT 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 145 ATCGGGCTTACCGCTTCCCTGGCTTGGGTGTGTGACAAACGCAACGCGCACGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGCGTGTGCGGAGCGCTCCGGCGCAAGTCTCGGATCTCCACCGCGACGTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCGCGTTCGACGGCGCTCCGATCACTCGGCCACCGCATGCGGACGCGCTTAAC 324
QY 101 GlyHisHisProGlyAspValIleSerValThrTyrGlnThrIleValThrArg 120
Db 325 GGGCATCATCCGCTGAGCTCATCTCGTGCACCTGGCAACCAAGTCGGCGCGACGCT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
```

US-09-684-215B-23 (1-128) x AAL40771 (1-1742)

QY	1	ThrAlaAlaSerAspAsnPhcInleuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle	20
DB	25	ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC	84
QY	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis	40
DB	85	GGGCGAGCGGATCGCATCGCGGCGCAGATCCGATCGGTGGGGGTCAACCCACCGTTCA	144
QY	41	IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg	60
DB	145	ATCGGGCTTACCGCTTCTCGCTTGGGTGTGTCGACAAACAAACGCGGCGACGCA	204
QY	61	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	80
DB	205	GTCCACACGGTGGTCCGGAGCGCTCCGGGGCAGTCTCGGCATCTCCACCGGGACGTG	264
QY	81	IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn	100
DB	265	ATCAGCGCGTCCGAGCGCTCCGATCAACTCGGCGCACCGGATGGCGGACGCGTTAAC	324
QY	101	GlyHisHisProGlyAspValIleSerValThrTTPGlnThrLysSerGlyGlyThrArg	120
DB	325	GGGCAATCATCCCGTGACGTCTCTCGGTGACCTGGCAACCAACAGTCCGGGCGCACGGT	384
QY	121	ThrGlyAsnValThrLeuAlaGlu	128
DB	385	ACAGGGAACGTGACATTTGGCCGAG	408

RESULT 14
AAL40768
ID AAL40768 standard; DNA; 1871 BP.
XX
AC AAL40768;
XX
XX
DT 03-OCT-2002 (first entry)
XX
DE Nucleotide sequence encoding MTB32A protein.
XX
KW Ra12; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
KW immunogen; cytokine; gene; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT CDS 89..1156
FT /*tag= a
FT /product= "Bacillus mycobacterium MTB32A protein"
XX
XX WO200125401-A2.
XX
PD 12-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US027652.
XX
XX 07-OCT-1999; 99US-0158585P.
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Guderian J;
XX
XX WPI; 2001-266299/27.
XX
XX P-PSDB; AAC22137.
XX
XX
XX Recombinant nucleic acid molecule for producing high yield expression of
XX desired fusion polypeptides, encodes fusion polypeptide comprising
XX Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
XX
XX Disclosure; Fig 1; 39pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a

395 ACAGGGAACGTGACATTTGGCCGAG 408

DB
RESULT 13
AAL40771
ID AAL40771 standard; DNA; 1742 BP.
XX
AC AAL40771;
XX
DT 03-OCT-2002 (first entry)
XX
DE Nucleotide sequence encoding Ra12-WT1 fusion protein.
XX
KW Ra12; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
KW immunogen; cytokine; gene; ds.
XX
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 4..1740
FT /*tag= a
FT /product= "Ra12-WT1 fusion protein"
XX
XX WO200125401-A2.
XX
PD 12-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US027652.
XX
XX 07-OCT-1999; 99US-0158585P.
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Guderian J;
XX
XX WPI; 2001-266299/27.
XX
XX P-PSDB; AAC22140.
XX
XX Recombinant nucleic acid molecule for producing high yield expression of
XX desired fusion polypeptides, encodes fusion polypeptide comprising
XX Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
XX
XX Disclosure; Fig 4; 39pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
XX fusion polypeptide, comprising a polynucleotide sequence of Ra12, a 14
XX kDa C-terminal fragment of serine protease antigen MTB32A of
XX Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
XX The recombinant fusion nucleic acids and polypeptides are useful for
XX providing stable and high yield expression of fusion polypeptides of both
XX eukaryotic and prokaryotic origin and to encode a protein product for use
XX as an antigen for detecting serum antibodies. The presence of serum
XX antibodies to M. tuberculosis antigens in an individual indicates that
XX the individual is infected with it. The fusion polypeptides are useful as
XX sources of proteins for monitoring binding of serum antibodies to fusion
XX proteins and as an immunogen to induce and/or enhance immune responses.
XX The coding sequences can be ligated with a coding sequence of another
XX molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
XX can be used in vivo as a DNA vaccine. This polynucleotide sequence
XX represents the DNA encoding the Ra12-WT1 fusion protein
XX
XX Sequence 1742 BP; 372 A; 569 C; 490 G; 311 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 5.4e-54 Length: 1742
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
CC kDa C-terminal fragment of serine protease antigen MTB32A of
CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
CC The recombinant fusion nucleic acids and polypeptides are useful for
CC providing stable and high yield expression of fusion polypeptides of both
CC eukaryotic and prokaryotic origin and to encode a protein product for use
CC as an antigen for detecting serum antibodies. The presence of serum
CC antibodies to M. tuberculosis antigens in an individual indicates that
CC the individual is infected with it. The fusion polypeptides are useful as
CC sources of proteins for monitoring binding of serum antibodies to fusion
CC proteins and as an immunogen to induce and/or enhance immune responses.
CC The coding sequences can be ligated with a coding sequence of another
CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
CC can be used in vivo as a DNA vaccine. This polynucleotide sequence
CC represents the DNA encoding the Mycobacterium tuberculosis MTB32A protein
XX
SQ Sequence 1871 BP; 317 A; 617 C; 605 G; 332 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,87e-54 Length: 1871
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x AAL40768 (1-1871)

QY 1 ThrAlaAlaSerAspAsnPhedInLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 758 ACAGCGCGTCCGATTAATTCAGATGTCACAGGGTGGCAGGATTCGCCATTCGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 818 GGGCAGGCGATGCGATCGCGGCGAAATCCGATCGGGTGGGGGTCAACCCACCGTTCCAT 877
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
DB 878 ATCCGGCGCTTACCGCTTCCTCGCTGGTGTGTGCGAACACAGCGACGCGCACGA 937
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 938 GTCCACAGCGGTGTCGGAAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 998 ATCAGCGCGTTCGAGCGGCTCCGATCACTCGGCGACGCGATGCGGACGCGCTTAAC 1057
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 1058 GGGCATCATCCGGTGACGTCTATCTCGTGACCTGGCAACCAAGTCTCGGGGCGACGCGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 1118 ACAGGAGACGTGACATGCGCGAG 1141

RESULT 15
ID ADA26353 standard; DNA; 2181 BP.
AC ADA26353;
XX ADA26353;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mycobacterium MTB32-MTB39f fusion protein encoding DNA.
XX
KW ds; gene; fusion polypeptide; MTB32A; MTB39; antigen; MTB32A; MTB39;
KW MTB85A; tuberculosis; tuberculostatic; gene therapy; vaccine.
XX
OS Chimeric.
OS Mycobacterium sp.
XX
XX
XX Key Location/Qualifiers

FT CDS 4. .2175
FT /*tag= a
FT /product= "MTB32-MTB39f fusion polypeptide"
PN MO2003070187-A2.
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-US004903.
XX
XX 15-FEB-2002; 2002US-0357351P.
XX (CORI-) CORIXA CORP.
XX Skeiky Y, Guderian J, Reed S;
XX WPI; 2003-697554/66.
XX P-PSDB; ADA26354.
XX
XX New isolated nucleic acid encoding a fusion polypeptide with the MTB32A
XX and MTB39 antigens, with or without the MTB85A antigen, from a
XX Mycobacterium species, useful for diagnosing, preventing and/or treating
XX tuberculosis infection.
XX
XX Claim 1; Fig 1; 112pp; English.
XX
XX The invention relates to a novel nucleic acid encoding a fusion
XX polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and
XX MTB85A antigen from a Mycobacterium species of the tuberculosis complex.
XX A polypeptide of the invention has tuberculostatic activity. A
XX polynucleotide of the invention may have a use in gene therapy, and as a
XX vaccine. The methods and compositions of the present invention are useful
XX for diagnosing, preventing and/or treating tuberculosis infection. The
XX present sequence is used in the exemplification of the invention.
XX
SQ Sequence 2181 BP; 341 A; 693 C; 792 G; 355 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7,01e-54 Length: 2181
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-684-215B-23 (1-128) x ADA26353 (1-2181)

QY 1 ThrAlaAlaSerAspAsnPhedInLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 598 ACAGCGCGTCCGATTAATTCAGATGTCACAGGGTGGCAGGATTCGCCATTCGATC 657
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 658 GGGCAGGCGATGCGATCGCGGCGCAAGTCTCGGCATCTCCACCGCTTCAT 717
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAsnGlyAlaArg 60
DB 718 ATCGGCGCTACCGCTTCCTCGGCTTGGGTGTTGTGCAACACACGCGCACGA 777
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 778 GTCCACAGCGTGTGTCGAGGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 837
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 838 ATCAGCGCGTTCGAGCGGCTCCGATCACTCGGCGCACCGCGATGCGGACGCGCTTAAC 897
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 998 GGGCATCATCCGGTGACGTCTATCTCGTGACCTGGCAACCAAGTCTCGGGGCGACGCGT 957
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB

Db	958	ACAGGGAACGTGACATTCGCCGAG	981
RESULT 16			
AAD47084			
ID	AAD47084	standard; DNA; 2190 BP.	
XX			
AC	AAD47084;		
XX			
DT	29-AUG-2003	(revised)	
DT	27-JAN-2003	(first entry)	
XX			
DE	Mycobacterium sp. MTB72FmutSA fusion protein encoding DNA.		
XX			
KW	Vaccine; immunity; diagnostic agent; gene therapy; TBH9; antigen;		
KW	Ra35MutSA; Ra12; MTB72MutSA; chimeric; gene; ds.		
XX			
OS	Mycobacterium sp.		
OS	Mycobacterium tuberculosis.		
OS	Chimeric.		
XX			
Key	Location/Qualifiers		
FT	1..2190		
FT	/tag= a		
FT	/product= "MTB72FmutSA fusion protein"		
XX			
PN	WO200272792-A2.		
XX			
PD	19-SEP-2002.		
XX			
PF	13-MAR-2002; 2002WO-US008223.		
XX			
PR	13-MAR-2001; 2001US-0275837P.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Skeiky Y, Brannon M, Guderian J;		
XX			
DR	WPI; 2002-759844/82.		
DR	P-PSDB; AA29709.		
XX			
PT	New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF,		
PT	M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity		
PT	against pathogenic microorganisms e.g. Leishmania and Mycobacterium		
PT	tuberculosis.		
XX			
PS	Disclosure; Page 92-93; 155pp; English.		
XX			
CC	The invention relates to a recombinant nucleic acid molecule encoding a		
CC	fusion polypeptide. The recombinant nucleic acid comprises a heterologous		
CC	polynucleotide sequence encoding an antigen or an antigenic fragment from		
CC	Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a		
CC	polypeptide or its fragment. The Leishmania polynucleotide is selected		
CC	from TSA, LeIF, M15, and 6H polynucleotides. Sequences of the invention		
CC	are used in methods for eliciting immune response in mammals. They are		
CC	useful as vaccines to elicit protective immunity against pathogenic		
CC	microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion		
CC	polypeptides are used for enhancing the expression of polynucleotides, as		
CC	in vivo diagnostic agents and for raising antibodies in a non-human		
CC	animal. The invention is used in gene therapy. The present sequence is a		
CC	DNA encoding MTB72F fusion protein. This fusion protein comprises		
CC	Ra35MutSA mutant protein and Ra12 protein from M. tuberculosis and TBH9		
CC	protein from Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS		
CC	field)		
XX			
SQ	Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	7.05e-54	Length:	2190
Score:	651.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-684-215B-23 (1-128) x AAD47084 (1-2190)

Qy	1	ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle	20
Db	22	ACGGCGCGCTCCGATAAATTCACAGCTGTCCAGGGTGGGACGGATTGCCATTCGGATC	81
Qy	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis	40
Db	82	GGGACGGCATGGCGATCCGGGCGCAGATCCGATCGGGTGGGGGTCCACCCACCGTTCAT	141
Qy	41	IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg	60
Db	142	ATCGGGCTACCGCTTCCTCGGCTGGGTGTGTGACACACACACGGCAACGGCGCAGCA	201
Qy	61	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	80
Db	202	GTCCAAACGGTGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTG	261
Qy	81	IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn	100
Db	262	ATCACCGCGGTGACGGCGCTCCGATCACTCGGCCACCGCGATGGCGACGGCTTAAC	321
Qy	101	GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyThrArg	120
Db	322	GGGCATCATCCCGGTGACGTCTCGTGACCTGCGCAACCAAGTCGGCGCGCACGCGT	381
Qy	121	ThrGlyAsnValThrLeuAlaGlu	128
Db	382	ACAGGGAACGTGACATTCGCCGAG	405

RESULT 17

AAD28343
ID AAD28343 standard; DNA; 2190 BP.

XX AAD28343;

XX 22-APR-2002 (first entry)

DE Mycobacterium species MTB72FmutSA fusion protein encoding DNA.

KW Fusion protein; antigen; serological sensitivity; immune response;
KW tuberculosis; infection; vaccines; MTB72FmutSA; Ra12-TbH9-Ra35MutSA;
KW mutant; mutein; ds.

XX Mycobacterium sp.

Key	Location/Qualifiers
FT CDS	1..2190
FT	/tag= a
FT	/product= "MTB72FmutSA fusion protein"
FT misc_feature	22..417
FT	/tag= b
FT misc_feature	/note= "Ra12 DNA fragment"
FT	424..1596
FT	/tag= c
FT misc_feature	/note= "TBH9FL DNA fragment"
FT	1603..2187
FT	/tag= d
FT	/note= "Ra35 DNA fragment"
FT mutation	replace(2128, T)
FT	/tag= e
XX	WO200198460-A2.
XX	27-DEC-2001.
XX	20-JUN-2001; 2001WO-US019959.
XX	20-JUN-2000; 2000US-00597796.
XX	01-FEB-2001; 2001US-0265737P.
XX	(CORI-) CORIXA CORP.

XX Skeiky Y, Reed S, Alderson M;
XX WPI; 2002-147798/19.
XX P-PSDB; AAE17573.
XX Composition comprising MTB39 antigen and MTB32A antigen from
XX Mycobacterium species, useful for eliciting immune response in a subject.
XX Claim 81; Page 108-109; 136pp; English.
XX The present invention relates to fusion proteins containing at least two
XX Mycobacterium species antigens, nucleotides encoding them and
XX compositions comprising such fusion proteins. The present invention
XX particularly relates to nucleic acids encoding fusion proteins that
XX include two or more individual M. tuberculosis antigens which increase
XX the serological sensitivity of sera from individuals infected with
XX tuberculosis and methods for their use in diagnosis, prevention and
XX treatment of tuberculosis infection. Sequences of the invention are
XX useful for eliciting an immune response in a mammal, e.g., human,
XX immunised with BCG. They are useful in the diagnosis, treatment and
XX prevention of Mycobacterium infection. The fusion proteins and the
XX polynucleotides are useful as diagnostic tools in patients infected with
XX Mycobacterium, in vitro and in vivo assays for detecting humoral
XX antibodies or cell-mediated immunity against M. tuberculosis, for the
XX diagnosis of an infection or monitoring of disease progression, as
XX immunogens to generate or elicit a protective immune response in a
XX patient and for raising anti-M. tuberculosis antibodies in a non-human
XX animal. Sequences of the invention are also used as vaccines. MTB32A
XX fusion proteins of the invention are useful as in vivo diagnostic agents
XX for intradermal skin test. The present sequence is a DNA encoding
XX Mycobacterium species MTB72FmutSA (Ra12-TbH9-Ra35MutSA) mutant fusion
XX protein
XX Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7,05e-54 Length: 2190
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-23 (1-128) x AAD28343 (1-2190)
Qy 1 ThrAlaAlaSerAspAsnPhcGlnSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGGTGGCGAGGATTCGCATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGGCGATCGCATCGCGGCCAGATCCGATCGGGTGGGGGTCAACCCACCGTTCAT 141
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyValAlaArg 60
Db 142 ATCGGGCCCTACCGCCCTTCCTCGGCTGGGTGTGTGCGACACACCGCAACGGCGCAGGA 201
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyValIleSerThrGlyAspVal 80
Db 202 GTCCACGCGTGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGCGAGTG 261
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 262 ATCACCGCGGTGACGGCGCTCCGATCACTCGGCCACCGCATCGCGGACGCGCTTAAC 321
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 322 GGGCATCATCCGGTGACGTCATCTCGTGACCTGGCAACCAAGCTCGGGCGGCACGGT 381
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 382 ACAGGAACGTCACATTGGCCGAG 405

RESULT 18
AAL40773
ID AAL40773 standard; DNA; 2191 BP.
XX
XX AAL40773;
AC
XX 03-OCT-2002 (first entry)
XX
XX Nucleotide sequence encoding Ra12-H9-32A fusion protein.
DE
XX
XX Ra12; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
XX vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
XX immunogen; cytokine; gene; ds.
XX
XX Unidentified.
OS
XX Chimeric.
FH Key Location/Qualifiers
FT CDS 1..2190
FT /tag= a
FT /product= "Ra12-H9-32A fusion protein"
XX
XX WO200125401-A2.
PN
XX
XX 12-APR-2001.
PD
XX
XX 06-OCT-2000; 2000WO-US027652.
PF
XX
XX 07-OCT-1999; 99US-0158585P.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Skeiky Y, Guderian J;
PI
XX
XX WPI; 2001-266299/27.
DR
XX
XX P-PSDB; AAO22142.
DR
XX
XX Recombinant nucleic acid molecule for producing high yield expression of
XX desired fusion polypeptides, encodes fusion polypeptide comprising
XX Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
XX
XX Disclosure; Fig 6; 39pp; English.
XX
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
XX fusion polypeptide, comprising a polynucleotide sequence of Ra12, a 14
XX kDa C-terminal fragment of serine protease antigen MTB32A of
XX Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
XX The recombinant fusion nucleic acids and polypeptides are useful for
XX providing stable and high yield expression of fusion polypeptides of both
XX eukaryotic and prokaryotic origin and to encode a protein product for use
XX as an antigen for detecting serum antibodies. The presence of serum
XX antibodies to M. tuberculosis antigens in an individual indicates that
XX the individual is infected with it. The fusion polypeptides are useful as
XX sources of proteins for monitoring binding of serum antibodies to fusion
XX proteins and as an immunogen to induce and/or enhance immune responses.
XX The coding sequences can be ligated with a coding sequence of another
XX molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
XX can be used in vivo as a DNA vaccine. This polynucleotide sequence
XX represents the DNA encoding the Ra12-H9-32A fusion protein
XX
XX Sequence 2191 BP; 340 A; 697 C; 797 G; 356 T; 0 U; 1 Other;
SQ

Alignment Scores:
Pred. No.: 7,05e-54 Length: 2191
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-23 (1-128) x AAL40773 (1-2191)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20
 DB 22 ACAGCGCGGTCCGATTAACATCCAGGTGTCAGAGGTGGCGAGGATTCGCATTCGGATC 81
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 DB 82 GGGCAGGCGATGCGATCCGGGCGAGATCCGATCGGTGGGGGTCAACCCACCGTTTCA 141
 QY 41 IleGlyProThrAlaPhaLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
 DB 142 ATCGGGCTACCGCTTCCTCGCTTGGTGTGTGTCGACAAACACGGCAACGGCGCAG 201
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 202 GTCCAAACGCGTGGTCCGAGAGCGCTCCGGCGGAGTCTCGCATCTCCACCGGCGAGTG 261
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 DB 262 ATCAGCGCGGTGACGGCGCTCCGATCAACTCGGCGACCGCGATGGCGAGCGCTTAAC 321
 QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
 DB 322 GGGCATCATCCCGGTGAGTCACTTCGGTGACCTCGGCAACCAAGTGGGGCGGACCGGT 381
 QY 121 ThrGlyAsnValThrLeuAlaGlu 128
 DB 382 ACAGGGAACGTGACATTCGCCGAG 405
 RESULT 19
 ABK14128
 ID ABK14128 standard; DNA; 2286 BP.
 XX AC ABK14128;
 XX 29-AUG-2003 (revised)
 XX 08-MAY-2002 (first entry)
 XX DNA encoding antigenic fusion protein Ra12-TbH9-Ra35 (Mtb32-Mtb39).
 XX Fused protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;
 KW tuberculostatic; immunogen; vaccine; Mtb32-Mtb39; Ra12; TbH9; Ra35;
 KW Ra12-TbH9-Ra35.
 XX Mycobacterium tuberculosis.
 OS Chimeric.
 XX FH Key Location/Qualifiers
 FT CDS 42..2231
 FT /tag= a
 FT /product= "Mtb32-Mtb39"
 FT /transl_except= (pos:498..506, aa:Asn-Ala)
 FT /transl_except= (pos:597..605, aa:Ala-Gln)
 FT /transl_except= (pos:798..802, aa:Ala)
 FT /note= "This codon has an apparent 2 nucleotide insertion
 FT which alters the reading frame"
 XX US2002009459-A1.
 XX 24-JAN-2002.
 XX 07-APR-1999; 99US-00287849.
 XX 13-MAR-1997; 97US-00818112.
 XX 01-OCT-1997; 97US-00942578.
 XX 18-FEB-1998; 98US-00025197.
 XX 07-APR-1998; 98US-00056556.
 XX 30-DEC-1998; 98US-00223040.
 XX (REED/) REED S G.
 XX (SKEI/) SKEIKY Y A.
 XX (DILL/) DILLON D C.
 XX (ALDE/) ALDERSON M.
 XX (CAMP/) CAMPOS-NETO A.

XX FI Reed SG, Skeiky YA, Dillon DC, Alderson M, Campos-Neto A;
 XX WPI; 2002-171134/22.
 XX P-PSDB; AAU74588.
 XX New fusion proteins of Mycobacterium tuberculosis antigens, useful for
 PT diagnosing, treating or preventing M. tuberculosis infection.
 PT Particularly as vaccine for treating or preventing tuberculosis.
 XX Example; Fig 1; 62pp; English.
 XX The invention relates to a purified polypeptide which induces an immune
 CC response of Mycobacterium tuberculosis. Polypeptides of the invention are
 CC useful for diagnosing, treating or preventing M. tuberculosis infection,
 CC particularly tuberculosis infection. In particular, the polypeptides are
 CC useful as a vaccine formulation with an adjuvant to afford long-term
 CC protection in animals against the development of tuberculosis. The
 CC protein coding sequence may be used to encode a protein product for use
 CC as an immunogen to induce and/or enhance an immune response to M.
 CC tuberculosis. This sequence represents DNA encoding an M. tuberculosis
 CC fusion protein of the invention. (Updated on 29-AUG-2003 to standardise
 CC OS field)
 XX SQ Sequence 2286 BP; 373 A; 719 C; 807 G; 381 T; 0 U; 6 Other;
 Alignment Scores:
 Pred. No.: 7,41e-54 Length: 2286
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-684-215B-23 (1-128) x ABK14128 (1-2286)
 QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 63 ACAGCGCGGTCCGATTAACATCCAGGTGTCAGAGGTGGCGAGGATTCGCATTCGGATC 122
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 DB 123 GGGCAGGCGATGCGATTCGGGCGCAGATCCGATCGGTGGGGGTCAACCCACCGTTTCA 182
 QY 41 IleGlyProThrAlaPhaLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
 DB 183 ATCGGGCTACCGCTTCCTCGCTTGGTGTGTGTCGACAAACACGGCAACGGCGCAGCG 242
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 243 GTCCAAACGCGTGGTCCGAGAGCGCTCCGGCGGCAAGTCTCGCATCTCCACCGGCGAGTG 302
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 DB 303 ATCAGCGCGGTGACGGCGCTCCGATCAACTCGGCGACCGCGATGGCGAGCGCGCTTAAC 362
 QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
 DB 363 GGGCATCATCCCGGTGAGTCACTTCGGTGACCTCGGCAACCAAGTGGGGCGGCGCGGT 422
 QY 121 ThrGlyAsnValThrLeuAlaGlu 128
 DB 423 ACAGGGAACGTGACATTCGCCGAG 446
 RESULT 20
 AAZ20194
 ID AAZ20194 standard; DNA; 2287 BP.
 XX AC AAZ20194;
 XX 17-JAN-2000 (first entry)
 XX Mycobacterium tuberculosis antigen fusion protein Mtb32A DNA.

XX Tuberculosis; antigen; fusion protein; Mtb32A; Ra12; TBH9; Ra35;
 XX diagnosis; therapy; vaccine; immunogen; ss.
 XX Mycobacterium tuberculosis.
 XX Key Location/Qualifiers
 XX CDS 42..2231
 XX /*tag= a
 XX
 XX WO9951748-A2.
 XX
 XX 14-OCT-1999.
 XX
 XX 07-APR-1999; 99WO-US007717.
 XX
 XX 07-APR-1998; 98US-00056556.
 XX
 XX 30-DEC-1998; 98US-00223040.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Skeiky YAW, Alderson M, Campos-Neto A;
 XX
 XX WPI; 1999-601610/51.
 XX
 XX P-PSDB; AAY32059.
 XX
 XX New fusion proteins useful for diagnosis, prevention and treatment of
 XX tuberculosis.
 XX
 XX Example; Fig 1A-B; 83pp; English.
 XX
 XX This DNA sequence includes a coding region for a recombinant
 XX Mycobacterium tuberculosis tri-antigen fusion protein (see AAY32059),
 XX termed Mtb32A, composed of the antigens Ra12, TBH9 and Ra35. The DNA is
 XX useful for the recombinant production of the fusion protein. Coding
 XX sequences for the antigens were modified by PCR in order to facilitate
 XX their fusion and subsequent expression of the fusion protein. 3 Coding
 XX sequences for Ra12, TBH9 and Ra25 were ligated to encode Mtb32A. The
 XX invention provides fusion proteins (see AAY32059-71) containing at least
 XX 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides
 XX encoding them are useful as vaccines for preventing tuberculosis
 XX (claimed), for diagnosis (via in vitro assays or intradermal skin tests
 XX for detection of anti-M. tuberculosis antibodies), monitoring of disease
 XX progression, and treatment of tuberculosis. They are more effective
 XX immunogens than mixtures of the individual protein components
 XX
 XX SQ Sequence 2287 BP; 374 A; 723 C; 805 G; 382 T; 0 U; 3 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 7.41e-54 Length: 2287
 XX Score: 651.00 Matches: 128
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 2 Gaps: 0
 XX
 XX US-09-684-215B-23 (1-128) x AAZ20194 (1-2287)
 XX
 XX QY 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlnGlyPheAlaIleProle 20
 XX
 XX Db 63 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGTGGCGGAGGATTCGCCATCCGATC 122
 XX
 XX QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 XX
 XX Db 123 GGGCAGCGGATGCGGATCGCGGCCAGATCCGATCGGGTGGGGGTACCCACCGTTTAT 182
 XX
 XX QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
 XX
 XX Db 183 ATCGGCGCTACCGCTTCTCGCTTGGTGTGTGTCGACACACGCAACGCGCACGA 242
 XX
 XX QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerIleuGlyIleSerThrGlyAspVal 80
 XX
 XX Db 243 GTCCACACGCGTGTGCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACG 302

QY 81 IleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 Db 303 ATCACCGCGGTGCGAGCGGCTCCGATCAACTCGGCCACCGCATGCGGACGCGTTAAC 362
 QY 101 GlyHisHisProGlyAspValIleSerValThrTrrpGlnThrLysSerGlyGlyThrArg 120
 Db 363 GGGCATCATCCCGGTGACGTGATCTCGGTGACCTGGCAACCAAGTCGGGCGGACGGGT 422
 QY 121 ThrGlyAsnValThrIleuAlaGlu 128
 Db 423 ACAGGGAACGTGACATTGGCCGAG 446
 RESULT 21
 AAD47083
 ID AAD47083 standard; DNA; 2287 BP.
 XX
 XX AAD47083;
 XX
 XX 29-AUG-2003 (revised)
 XX 27-JAN-2003 (first entry)
 XX
 XX Mycobacterium sp. MTB72F fusion protein encoding DNA.
 XX
 XX Vaccine; immunity; diagnostic agent; gene therapy; TBH9; antigen; Ra35;
 XX Ra12; MTB72F; chimeric; gene; ds.
 XX
 XX Mycobacterium sp.
 XX Mycobacterium tuberculosis.
 XX Chimeric.
 XX
 XX Key Location/Qualifiers
 XX CDS 42..2231
 XX /*tag= a
 XX /product= "MTB72F fusion protein"
 XX
 XX WO200272792-A2.
 XX
 XX 19-SEP-2002.
 XX
 XX 13-MAR-2002; 2002WO-US008223.
 XX
 XX 13-MAR-2001; 2001US-0275837P.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 XX Skeiky Y, Brannon M, Guderian J;
 XX
 XX WPI; 2002-759844/82.
 XX P-PSDB; AAE29708.
 XX
 XX New recombinant nucleic acid molecule comprising a Leishmania TSA, Leif,
 XX M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
 XX against pathogenic microorganisms e.g. Leishmania and Mycobacterium
 XX tuberculosis.
 XX
 XX Disclosure; Page 87-90; 155pp; English.
 XX
 XX The invention relates to a recombinant nucleic acid molecule encoding a
 XX fusion polypeptide. The recombinant nucleic acid comprises a heterologous
 XX polynucleotide sequence encoding an antigen or an antigenic fragment from
 XX Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
 XX polypeptide or its fragment. The Leishmania polynucleotide is selected
 XX from TSA, Leif, M15, and 6H polynucleotides. Sequences of the invention
 XX are used in methods for eliciting immune response in mammals. They are
 XX useful as vaccines to elicit protective immunity against pathogenic
 XX microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
 XX polypeptides are used for enhancing the expression of polynucleotides, as
 XX in vivo diagnostic agents and for raising antibodies in a non-human
 XX animal. The invention is used in gene therapy. The present sequence is a
 XX DNA encoding MTB72F fusion protein. This fusion protein comprises Ra12
 XX and Ra35 protein from Mycobacterium tuberculosis and TBH9 protein from
 XX Mycobacterium sp. (Updated on 29-AUG-2003 to standardise OS field)

CC polynucleotide of the invention may have a use in gene therapy, and as a
 CC vaccine. The methods and compositions of the present invention are useful
 CC for diagnosing, preventing and/or treating tuberculosis infection. The
 CC present sequence is used in the exemplification of the invention.

SQ Sequence 2487 BP; 394 A; 784 C; 896 G; 413 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,176-54 Length: 2487
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-684-215B-23 (1-128) x ADA26359 (1-2487)

Qy 1 ThrAlaAlaSerAspAsnPhedInLeuSerGlnGlyGlnGlyPheAlaIleProile 20
 Db 25 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGCTGGGAGGATTCGCCATTCCGATC 84
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
 Db 85 GGGCAGGCGATGGCGATCGCGGCGAGATCCGATCGGGTGGGGGTCAACCACCGTTTCAT 144
 Qy 41 IleGlyProThrAlaPheLeuGlyLeuValValAspAsnGlyValAlaArg 60
 Db 145 ATCGGCGCTACCGCTTCTCGGCTGGTGTGTCGACACACGCGGACGCGGACGCA 204
 Qy 61 ValGlnArgValValGlySerAlaProAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 205 GTTCAACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGCGT 264
 Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 Db 265 ATCAGCGGTCGACGCGCTCCGATCACTCGGCGACGCGATGCGGACGCGCTTAAC 324
 Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 Db 325 GGGCATCATCCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGGCGCGGT 384
 Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
 Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 25

ADA26358

ID ADA26358 standard; DNA; 2637 BP.

AC ADA26358;

XX 20-NOV-2003 (first entry)

DE Mycobacterium MTB72F-Erd14 (fusion MTB89F) protein encoding DNA.

XX ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
 KW tuberculosis; tuberculostatic; gene therapy; vaccine.

XX Chimeric.

OS Mycobacterium sp.

XX Key

FT Location/Qualifiers

FT 4..2631

FT /tag= a

FT /product= "MTB72F-Erd14 (fusion MTB89F)"

XX WO2003070187-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-US004903.

XX 15-FEB-2002; 2002US-0357351P.

XX PF

XX DT

XX 29-AUG-2003 (revised)

XX 27-JAN-2003 (first entry)

XX DT

XX AC

XX AD47110;

XX ID

XX AD47110 standard; DNA; 2808 BP.

XX RESULT 26

XX AD47110

XX 385 ACAGGGAACGTGACATTGGCCGAG 408

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 385 ACAGGGAACGTGACATTGGCCGAG 408

XX

PA

XX

PI

XX

DR

XX

DR

XX

PT

XX

PT

XX

PT

XX

PS

XX

CC

XX

CC

XX

CC

XX

CC

XX

CC

XX

CC

XX

SQ

XX

Alignment Scores:

Pred. No.: 8,746-54 Length: 2637
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-684-215B-23 (1-128) x ADA26358 (1-2637)

Qy 1 ThrAlaAlaSerAspAsnPhedInLeuSerGlnGlyGlnGlyPheAlaIleProile 20
 Db 25 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGCTGGGAGGATTCGCCATTCCGATC 84
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
 Db 85 GGGCAGGCGATGGCGATCGCGGCGAGATCCGATCGGGTGGGGGTCAACCACCGTTTCAT 144
 Qy 41 IleGlyProThrAlaPheLeuGlyLeuValValAspAsnGlyValAlaArg 60
 Db 145 ATCGGCGCTACCGCTTCTCGGCTGGTGTGTCGACACACGCGGACGCGGACGCA 204
 Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 205 GTCCACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 264
 Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 Db 265 ATCAGCGGTCGACGCGCTCCGATCACTCGGCGACGCGATGCGGACGCGCTTAAC 324
 Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 Db 325 GGGCATCATCCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGGCGCGGT 384
 Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
 Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 26

ADA47110

ID ADA47110 standard; DNA; 2808 BP.

XX AD47110;

XX 385 ACAGGGAACGTGACATTGGCCGAG 408

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 385 ACAGGGAACGTGACATTGGCCGAG 408

DE	Mycobacterium sp. MTB72F-Leishmania sp. MAPS (aka r95f)-fusion DNA.
XX	Vaccine; immunity; diagnostic agent; gene therapy; MTB72F; MAPS;
XX	chimeric; gene; ds.
XX	
XX	Mycobacterium sp.
OS	Leishmania sp.
OS	Chimeric.
XX	
Key	Location/Qualifiers
FFH	4..2796
FT	/*tag= a
FT	/product= "Mycobacterium sp. MTB72F-Leishmania sp. MAPS
FT	(aka r95f) fusion protein"
XX	
WO	2002027292-A2..
EN	
XX	
PD	19-SEP-2002.
XX	
XX	13-MAR-2002; 2002WO-US008223.
XX	
XX	13-MAR-2001; 2001US-0275837P.
PR	
PA	(CORI-) CORIXA CORP.
PI	
PI	Skeiky Y, Brannon M, Guderian J;
XX	
DR	WPI; 2002-759844/82.
DR	P-P8DB; AAE29731.
XX	
XX	New recombinant nucleic acid molecule comprising a Leishmania TSA, LeifP,
PT	M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
PT	against pathogenic microorganisms e.g. Leishmania and Mycobacterium
PT	tuberculosis.
XX	
XX	Example 6; Page 128-129; 155pp; English.
XX	
CC	The invention relates to a recombinant nucleic acid molecule encoding a
CC	fusion polypeptide. The recombinant nucleic acid comprises a heterologous
CC	polynucleotide sequence encoding an antigen or an antigenic fragment from
CC	Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
CC	polypeptide or its fragment. The Leishmania polynucleotide is selected
CC	from TSA, LeifP, M15, and 6H polynucleotides. Sequences of the invention
CC	are used in methods for eliciting immune response in mammals. They are
CC	useful as vaccines to elicit protective immunity against pathogenic
CC	microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
CC	polypeptides are used for enhancing the expression of polynucleotides, as
CC	in vivo diagnostic agents and for raising antibodies in a non-human
CC	animal. The invention is used in gene therapy. The present sequence is
CC	Mycobacterium sp. MTB72F-Leishmania sp. thiol specific antioxidant [TSA;
CC	MAPS (aka r95f)] fusion DNA. This sequence comprises Mycobacterium sp.
CC	MTB72F (a 72 kDa poly-protein fusion construct comprising Ral2-TDH9-Ra35)
CC	linked to the Leishmania TSA (MAPS). (Updated on 29-AUG-2003 to
CC	standardise OS field)
XX	
XX	Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	9,4e-54 Length: 2808
Score:	651.00 Matches: 128
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	Gaps: 0
US-09-684-215B-23 (1-128) x AAD47110 (1-2808)	
Qy	1 ThrAlaAlaSerAspAsnPhedInLeuSerGlnGlyGlnGlyPheAlaIleProlle 20
Db	25 ACGGCCGCTCCGATAACTTCAGGTGCCAGGTGGCAGGATTTCGCAATTCGATC 84
Qy	21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40

XX Sequence 2808 BP; 466 A; 889 C; 982 G; 471 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9.4e-54 Length: 2808
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-684-215B-23 (1-128) x ADA26357 (1-2808)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 25 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCGAGGATTGCCATTCCGATC 84
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
 DB 85 GGGCAGGCGATGGCGATGGCGGCCAGATCCGATCGGTGGGGGTCAACCCACCGTTTCA 144
 QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
 DB 145 ATCGGCGCTACCGCTTCTCGCTTGGTGTGTGACAAACACGCGCAACGGCGCAGCA 204
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 205 GTCCAAACGCGTGGTGGGAGCGCTCGGCGGCAAGTCTCGGCATCTCCACCGGCGAGTG 264
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 DB 265 ATCACCGCGTGCAGCGCGCTCCGATCAACTCGGCACCGCGATGGCGAGCGCGTTAAC 324
 QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 DB 325 GGGCATCATCCCGGTGACGTATCTCGGTGACCTCGCAACCAAGTGGGGCGGCGCGT 384

QY 121 ThrGlyAsnValThrLeuAlaGlu 128
 DB 385 ACAGGGAACGTGACATTGCCCGAG 408

RESULT 28

ADA26355
 ID ADA26355 standard; DNA; 3030 BP.

XX AC
 XX ADA26355;

XX DT 20-NOV-2003 (first entry)

XX Mycobacterium MTB-102F fusion protein encoding DNA.

XX KW db; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
 XX tuberculosi; tuberculosi; gene therapy; vaccine.

OS Chimeric.

OS Mycobacterium sp.

XX FH Key Location/Qualifiers
 FT CDS 1..3030
 FT /*tag= a
 FT /product= "MTB-120F fusion protein"
 FT /note= "No stop codon given"

XX PN WO2003070187-A2.

XX PD 28-AUG-2003.

XX PF 18-FEB-2003; 2003WO-US004903.

XX PR 15-FEB-2002; 2002US-0357351P.

XX PA (CORI-) CORIXA CORP.

PI Skeiky Y, Guderian J, Reed S;
 XX WPI; 2003-697554/56.
 DR P-PSDB; ADA26356.

XX New isolated nucleic acid encoding a fusion polypeptide with the MTB32A
 PT and MTB39 antigens, with or without the MTB85A antigen, from a
 PT Mycobacterium species, useful for diagnosing, preventing and/or treating
 PT tuberculosis infection.

XX Claim 5; Fig 3; 112pp; English.

XX The invention relates to a novel nucleic acid encoding a fusion
 CC polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and
 CC MTB85A antigen from a Mycobacterium species of the tuberculosis complex.
 CC A polypeptide of the invention has tuberculostatic activity. A
 CC polynucleotide of the invention may have a use in gene therapy, and as a
 CC vaccine. The methods and compositions of the present invention are useful
 CC for diagnosing, preventing and/or treating tuberculosis infection. The
 CC present sequence is used in the exemplification of the invention.

XX Sequence 3030 BP; 498 A; 966 C; 1062 G; 504 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.03e-53 Length: 3030
 Score: 651.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-684-215B-23 (1-128) x ADA26355 (1-3030)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 595 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCGAGGATTGCCATTCCGATC 654

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
 DB 655 GGGCAGGCGATGGCGATGGCGGCCAGATCCGATCGGTGGGGGTCAACCCACCGTTTCA 714

QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
 DB 715 ATCGGCGCTACCGCTTCTCGCTTGGTGTGTGACAAACACGCGCAACGGCGCAGCA 774

QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 775 GTCCAAACGCGTGGTGGGAGCGCTCGGCGGCAAGTCTCGGCATCTCCACCGCGCAGTG 834

QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 DB 835 ATCACCGCGTGCAGCGCGCTCCGATCAACTCGGCACCGCGATGGCGAGCGCGTTAAC 894

QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 DB 895 GGGCATCATCCCGGTGACGTATCTCGGTGACCTGGCAACCAAGTGGGGCGGCGCGT 954

QY 121 ThrGlyAsnValThrLeuAlaGlu 128
 DB 955 ACAGGGAACGTGACATTGCCCGAG 978

RESULT 29

ADA26363
 ID ADA26363 standard; DNA; 3060 BP.

XX AC ADA26363;

XX DT 20-NOV-2003 (first entry)

XX M. bovis MTB72F and 85b complex antigen (fusion MTB103F) DNA.

XX ds; gene; fusion protein; MTB32A; MTB39; antigen; MTB32A; MTB39; MTB85A;
 KW tuberculosi; tuberculostatic; gene therapy; vaccine; MTB72F; 85B.

XX	Chimeric.
OS	Mycobacterium bovis.
XX	
FH	Key Location/Qualifiers
FF	CDS 4..3054
FT	/+tag= a
FT	/product= "MTB72F and 85b complex (fusion MTB103F) "
XX	
PN	WO2003070187-A2.
XX	
PD	28-AUG-2003.
XX	
PF	18-FEB-2003; 2003WO-US004903.
XX	
PR	15-FEB-2002; 2002US-0357351P.
XX	(CORI-) CORIXA CORP.
XX	
PI	Skeiky Y, Guderian J, Reed S;
XX	
DR	WPI; 2003-697554/66.
DR	P-PSDB; ADA26370.
XX	
XX	New isolated nucleic acid encoding a fusion polypeptide with the MTB32A
PT	and MTB39 antigens, with or without the MTB85A antigen, from a
PT	Mycobacterium species, useful for diagnosing, preventing and/or treating
PT	tuberculosis infection.
XX	
XX	Claim 84; Fig 11; 112pp; English.
XX	
CC	The invention relates to a novel nucleic acid encoding a fusion
CC	polypeptide, comprising a MTB32A and MTB39 antigen, or MTB32A, MTB39 and
CC	MTB85A antigen from a Mycobacterium species of the tuberculosis complex.
CC	A polypeptide of the invention has tuberculostatic activity. A
CC	polynucleotide of the invention may have a use in gene therapy, and as a
CC	vaccine. The methods and compositions of the present invention are useful
CC	for diagnosing, preventing and/or treating tuberculosis infection. The
CC	present sequence is used in the exemplification of the invention.
XX	
SQ	Sequence 3060 BP; 503 A; 977 C; 1070 G; 510 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	Length: 3060
Score:	Matches: 128
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Best Local Similarity:	Mismatches: 0
Query Match:	Indels: 0
DB:	Gaps: 0
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Oy	1 ThrAlaAserAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Dd	25 ACGGCGGTCCGATTAACCTTCAGGTGCCAGGGTGGCAGGGATTTCGCATTCGCATC 84
Oy	21 GlyClnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Dd	85 GGGCAGCGCATGCGCATCGCGGCGCAGATCCGATCGGTGGGGGGTGTCACCACCGTTCAAT 144
Oy	41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyVsnGlyAlaArg 60
Dd	145 ATCGGGCTTACCGCCCTTCTCGGCTTGGTGTGTTCGACACACACACACACGGCACGCGCACGA 204
Oy	61 ValGlnArgValValGlySerAlaProAlaLaserLeuGlyIleSerThrGlyAspVal 80
Dd	205 GTCCACACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 264
Oy	81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Dd	265 ATCACCGCGTGCACGGCGCTCGATCAACTCGGCGACCGGATGGCGGACGGCGCTTAACTAAC 324
Oy	101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

Db 25 ACGCCCGCTCCGATACCTCCAGCTGTCCAGGGTGGGAGGGATTCCGCCATTCGGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 85 GGGCAGCGCATGGCGATCGGGGGCCAGATCCGATCGGGTGGGGGTCAACCACCGTTTCA 144
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaPheAsnAsnGlyAlaArg 60
Db 145 ATCGGGCTTACCGCTTCCCTCGGCTTGGGTGTTCGACAAACACGGCAACGGCGCACGA 204
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCACACGGGTGTTCGGGAGGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGGACGTG 264
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACC CGGTGCGACGGCGCTCCGATCACTCGGCCACCGCATGGCGGACGCGCTTAAC 324
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyThrArg 120
Db 325 GGGCATCATCCCGTGACGTATCTCGGTGACCTGGCAACCAAGTCGGCGGCGACCGGT 384
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGAACGTGACATTGGCGGAG 408

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	651	100.0	702	9	US-09-287-849-27	Sequence 27, Appl
2	651	100.0	702	15	US-10-359-460-27	Sequence 27, Appl
3	651	100.0	1002	15	US-10-098-732A-3	Sequence 3, Appl
4	651	100.0	1002	15	US-10-098-732A-5	Sequence 5, Appl
5	651	100.0	1068	9	US-09-712-363-15	Sequence 15, Appl
6	651	100.0	2181	16	US-10-369-983-1	Sequence 1, Appl
7	651	100.0	2190	15	US-10-098-732A-17	Sequence 17, Appl
8	651	100.0	2287	9	US-09-287-849-1	Sequence 1, Appl
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10	651	100.0	2287	15	US-10-098-732A-15	Sequence 15, Appl
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12	651	100.0	2451	16	US-10-369-983-8	Sequence 8, Appl
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14	651	100.0	2637	16	US-10-369-983-6	Sequence 6, Appl
15	651	100.0	2808	15	US-10-098-732A-64	Sequence 64, Appl
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18	651	100.0	3060	16	US-10-369-983-11	Sequence 11, Appl
19	651	100.0	3104	16	US-10-369-983-10	Sequence 10, Appl
20	651	100.0	3474	16	US-10-369-983-9	Sequence 9, Appl
21	646	99.2	447	15	US-10-193-002-4	Sequence 4, Appl
22	646	99.2	447	15	US-10-084-843-4	Sequence 4, Appl
23	646	99.2	447	15	US-10-098-732A-9	Sequence 9, Appl
24	646	99.2	1872	15	US-10-193-002-17	Sequence 17, Appl
25	646	99.2	1872	15	US-10-084-843-17	Sequence 17, Appl
26	646	99.2	1872	15	US-10-098-732A-1	Sequence 1, Appl
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28	608	93.4	675	9	US-09-780-669-822	Sequence 822, App
29	608	93.4	675	9	US-09-822-827-822	Sequence 822, App
30	608	93.4	675	9	US-09-895-793-822	Sequence 822, App
31	608	93.4	675	9	US-09-895-814-822	Sequence 822, App
32	608	93.4	675	14	US-10-012-896-822	Sequence 822, App
33	608	93.4	675	15	US-10-144-678A-822	Sequence 822, App
34	608	93.4	675	15	US-10-294-025-822	Sequence 822, App
35	608	93.4	822	9	US-09-736-457-1862	Sequence 1862, Ap
36	608	93.4	822	9	US-09-902-941-1862	Sequence 1862, Ap
37	608	93.4	822	9	US-09-849-626-1862	Sequence 1862, Ap
38	608	93.4	822	13	US-10-283-017-1862	Sequence 1862, Ap
39	608	93.4	822	15	US-10-017-754-1862	Sequence 1862, Ap
40	608	93.4	822	15	US-10-113-872-1862	Sequence 236, App
41	608	93.4	894	13	US-09-878-722-236	Sequence 236, App
42	608	93.4	894	13	US-09-904-456-236	Sequence 353, App
43	608	93.4	900	9	US-09-735-705-353	Sequence 353, App
44	608	93.4	900	9	US-09-850-716A-353	Sequence 353, App
45	608	93.4	900	9	US-09-897-778-353	Sequence 353, App

ALIGNMENTS

RESULT 1

US-09-287-849-27
; Sequence 27, Application US/09287849
; Patent No. US20020009459A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 09/056,556

APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 27
LENGTH: 702
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: bi-fusion
OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
OTHER INFORMATION: frame 1
NAME/KEY: CDS
LOCATION: (1)..(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(700)
OTHER INFORMATION: reading frame 2
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(701)
OTHER INFORMATION: reading frame 3
US-10-359-460-27

Alignment Scores:
Pred. No.: 3,4e-69 Length: 702
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-359-460-27 (1-702)

QY	1	ThrAlaAlaSerAspAsn	PheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle	20
Db	25	ACGGCCGCTCCGATTA	CTTCAGCTGCCAGGTTGGCAGGGATTCGCCATTCGGATC	84
QY	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis	40	
Db	85	GGGACGGGATGGCGATCGCGGCCAGATCCGATCGGTGGGGGTCA	144	
QY	41	IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg	60	
Db	145	ATCGGGCTACCGCTTCCTCGGCTGGGTGTTCGACAAACACACGGCAACGGCGACGA	204	
QY	61	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	80	
Db	205	GTCCACGGCTGGTTCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCCGCGTTCAT	264	
QY	81	IleThrAlaValAspGlyAlaProIleAenSerAlaThrAlaMetAlaAspAlaLeuAen	100	
Db	265	ATCACCGCGTTCGACGGCTTCGGATCAACTCGGCCCACTCGGATCGGCGGCGGCTTAAC	324	

PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 27
LENGTH: 702
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: bi-fusion
OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
OTHER INFORMATION: frame 1
NAME/KEY: CDS
LOCATION: (1)..(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
LOCATION: (2)..(700)
OTHER INFORMATION: reading frame 2
NAME/KEY: CDS
LOCATION: (3)..(701)
OTHER INFORMATION: reading frame 3
US-09-287-849-27

Alignment Scores:
Pred. No.: 3,4e-69 Length: 702
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-287-849-27 (1-702)

QY	1	ThrAlaAlaSerAspAsn	PheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle	20
Db	25	ACGGCCGCTCCGATTA	CTTCAGCTGCCAGGTTGGCAGGGATTCGCCATTCGGATC	84
QY	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis	40	
Db	85	GGGACGGGATGGCGATCGCGGCCAGATCCGATCGGTGGGGGTCA	144	
QY	41	IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg	60	
Db	145	ATCGGGCTACCGCTTCCTCGGCTGGGTGTTCGACAAACACACGGCAACGGCGACGA	204	
QY	61	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	80	
Db	205	GTCCACGGCTGGTTCGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCGGTG	264	
QY	81	IleThrAlaValAspGlyAlaProIleAenSerAlaThrAlaMetAlaAspAlaLeuAen	100	
Db	265	ATCACCGCGTTCGACGGCTTCGGATCAACTCGGCCCACTCGGATCGGCGGCGGCTTAAC	324	
QY	101	GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg	120	
Db	325	GGGCAATCATCCGGTGACGTCACTTCGGTGACCTGGCAACCAAGTGGGGCGGCGCGT	384	
QY	121	ThrGlyAsnValThrLeuAlaGlu	128	
Db	385	ACAGGGAAACGTGACATTTGCCCGAG	408	

RESULT 2
US-10-359-460-27
Sequence 27, Application US/10359460
Publication No. US2003014791A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.M.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio

QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 325 GGGCATCATCCGGTGACGTTCATTCGGTGACCTGGCAACCAAGTCCGGCGGACCGGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 3

US-10-098-732A-3
; Sequence 3, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Guderman, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Leishmania Antigen
; FILE REFERENCE: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ra35 mature
US-10-098-732A-3

Alignment Scores:
Pred. No.: 5,25e-69 Length: 1002
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-098-732A-3 (1-1002)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 598 ACGGCGCGTCCGATAACTTCAGCTGTCCAGGTGGCGAGGATTCCGCAATCCGATC 657
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 658 GGGCAGGCGATGGCGATCGGGCCAGATCCGATCGGGTGGGGGTACACCCACCGTTTCA 717
QY 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyAsnGlyAlaArg 60
Db 718 ATCGGCGCTTACCGCTTCTCGGTGGGTGTGTCGACAAACACGCAACGGCGCAGCA 777
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 778 GTCCAAACGGGTGTCGGGAGCGCTCCGGCGGCAAGTCTCCGATCTCCACCGGCGAGTG 837
QY 81 IleThrAlaValAspGlyValProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 838 ATCAACGGGTGTCAGCGCGCTCCGATCACTCGGCACCGCGATGGCGCGCTTAAC 897
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 898 GGGCATCATCCGGTGACGTTCATTCGGTGACCTGGCAACCAAGTCCGGCGGACCGGT 957
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 958 ACAGGGAACGTGACATTGGCCGAG 981

RESULT 4

US-10-098-732A-5
; Sequence 5, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Guderman, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Leishmania Antigen
; FILE REFERENCE: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ra35FLMutSA
US-10-098-732A-5

Alignment Scores:
Pred. No.: 5,25e-69 Length: 1002
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-098-732A-5 (1-1002)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 598 ACGGCGCGTCCGATAACTTCAGCTGTCCAGGTGGCGAGGATTCCGCAATCCGATC 657
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 658 GGGCAGGCGATGGCGATCGGGCCAGATCCGATCGGGTGGGGGTACACCCACCGTTTCA 717
QY 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyAsnGlyAlaArg 60
Db 718 ATCGGCGCTTACCGCTTCTCGGTGGGTGTGTCGACAAACACGCAACGGCGCAGCA 777
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 778 GTCCAAACGGGTGTCGGGAGCGCTCCGGCGGCAAGTCTCCGATCTCCACCGGCGAGTG 837
QY 81 IleThrAlaValAspGlyValProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 838 ATCAACGGGTGTCAGCGCGCTCCGATCACTCGGCACCGCGATGGCGCGCTTAAC 897
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 898 GGGCATCATCCGGTGACGTTCATTCGGTGACCTGGCAACCAAGTCCGGCGGACCGGT 957
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 958 ACAGGGAACGTGACATTGGCCGAG 981

RESULT 5

US-09-712-363-15
; Sequence 15, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1998-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1068
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-15

Alignment Scores:
Pred. No.: 5,678-69 Length: 1068
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-712-363-15 (1-1068)

Qy 1 ThrAlaAlaSerAspAsnPhgInLeuSerGInGlyGInGlyPheAlaIleProfile 20
Db 670 ACGCGCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 729

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 730 GGGCAGGCGATGGCGATCGCGGCGCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCAT 789

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArg 60
Db 790 ATCGGCGCTTACCGCTTCTCGGCTGTGGTGTGTCGACAAACGCGCAACGGCGACGA 849

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 850 GTCCACGCGTGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTG 909

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 910 ATCACCAGCGTGGCGGCGCTCCGATCACTCGGCCACCGGATGGCGGCGCGCTTAAC 969

Qy 101 GlyHisHisProGlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArg 120
Db 970 GGGCATCATCCGGTGACGTCTATCTCGGTGACCTCGGCAACCAAGTCCGGGCGGACGCGT 1029

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 1030 ACAGGAGCGTGACATGGCCGAG 1053

RESULT 6
US-10-369-983-1
Sequence 1, Application US/10359983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir

APPLICANT: Guderian, Jeff
APPLICANT: Reed, Steven
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2481
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: mutated
OTHER INFORMATION: MTB32-MTB39F fusion protein (MTB32MutSA)
US-10-369-983-1

Alignment Scores:
Pred. No.: 1,358-68 Length: 2181
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-369-983-1 (1-2181)

Qy 1 ThrAlaAlaSerAspAsnPhgInLeuSerGInGlyGInGlyPheAlaIleProfile 20
Db 598 ACGCGCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 657

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 658 GGGCAGGCGATGGCGATCGCGGCGCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCAT 717

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAspAsnGlyAsnGlyAlaArg 60
Db 718 ATCGGCGCTTACCGCTTCTCGGCTGTGGTGTGTCGACAAACGCGCAACGGCGACGA 777

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 778 GTCCACGCGTGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTG 837

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 838 ATCACCAGCGTGGCGGCGCTCCGATCACTCGGCCACCGGATGGCGGCGCGCTTAAC 897

Qy 101 GlyHisHisProGlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArg 120
Db 898 GGGCATCATCCGGTGACGTCTATCTCGGTGACCTCGGCAACCAAGTCCGGGCGGACGCGT 957

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 958 ACAGGAGCGTGACATGGCCGAG 981

RESULT 7
US-10-098-732A-17
Sequence 17, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837

;; PRIOR FILING DATE: 2001-03-13
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 17
;; LENGTH: 2190
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:MTB72FmutSA
;; OTHER INFORMATION: (Ra12-TbH9-Ra35mutSA)
US-10-098-732A-17

Alignment Scores:
Pred. No.: 1,36e-68 Length: 2190
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-098-732A-17 (1-2190)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGGTGGGAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGCGATGGCGATCGGGCCAGATCCGATCGGGTGGGGGTACCCACCGTTTCAT 141
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
Db 142 ATCGGGCTACCGCTTCTCCGGCTTGGTGTTCGACCAACACGCGACGCGACGA 201
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 202 GTCCAAACGCGTGGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGGCGAGCTG 261
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 262 ATCACCAGCGTGGCGGCTCCGATCACTCCGCCACCGCATGGCGGACGCGCTTAAC 321
Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 322 GGGCATCATCCGGTGAGTCTCATCTCGGTGACCTGGCAACCAAGTGGGCGGACGCGT 381
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 382 ACAGGGAACGTGACATTGGCCGAG 405

RESULT 8

US-09-287-849-1
; Sequence 1, Application US/09287849
; Patent No. US2002009459A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and Their Uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 09/056,556

;; PRIOR FILING DATE: 1998-04-07
;; PRIOR APPLICATION NUMBER: US 09/223,040
;; PRIOR FILING DATE: 1998-12-30
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 2287
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:tri-fusion
;; OTHER INFORMATION: protein Ra12-TbH9-Ra35 (designated MtB32-Mtb39
;; OTHER INFORMATION: fusion)
;; NAME/KEY: modified_base
;; LOCATION: (30)
;; OTHER INFORMATION: n = g, a, c or t
;; NAME/KEY: modified_base
;; LOCATION: (33)
;; OTHER INFORMATION: n = g, a, c or t
;; NAME/KEY: CDS
;; LOCATION: (42)..(2231)
;; NAME/KEY: modified_base
;; LOCATION: (2270)
;; OTHER INFORMATION: n = g, a, c or t
US-09-287-849-1

Alignment Scores:
Pred. No.: 1,43e-68 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-287-849-1 (1-2287)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 63 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGGTGGGAGGATTCGCCATTCCGATC 122
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 123 GGGCAGCGATGGCGATCGGGCCAGATCCGATCGGGTGGGGGTACCCACCGTTTCAT 182
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
Db 183 ATCGGGCTACCGCTTCTCCGGCTTGGTGTTCGACCAACACGCGACGCGACGA 242
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGGCGAGCTG 302
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 303 ATCACCAGCGTGGCGGCTCCGATCAACTCGGCCACCGCATGGCGGACGCGCTTAAC 362
Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 363 GGGCATCATCCGGTGAGTCTCATCTCGGTGACCTGGCAACCAAGTGGGCGGACGCGT 422
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTGGCCGAG 446

RESULT 9

US-10-359-460-1
; Sequence 1, Application US/10359460
; Publication No. US20030147911A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/287,849
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
OTHER INFORMATION: protein Ra12-TbH9-Ra35 (designated Mtb32-Mtb39)
OTHER INFORMATION: fusion)
FEATURE:
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
FEATURE:
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(2231)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2270)
OTHER INFORMATION: n = g, a, c or t
US-10-359-460-1
Alignment Scores:
Pred. No.: 1,43e-68 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-359-460-1 (1-2287)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 63 ACAGCCGCGTCCGATTAATCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 122
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 123 GGGCAGCGGATGCGGATCGGGCCAGATCCGATCCGGTGGGGGTACCCACCGTTCTAT 182
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAnglyAenGlyAlaArg 60
Db 183 ATCGGGCTACCGCTTCCTCGCTTGGGTGGTGTTCGACAAACCGCAACGGCGCACGA 242
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCACCGGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCACGTG 302
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

Db 303 ATCACCAGCGGTCCAGCGGCTCCGATCAATCGGCACCGGATGGCGGACCGCTTAAC 362
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 363 GGGCATATCCCGGTGAGGTATCTCGGTGACCTGGCAACCAAGTCGGGGCGCACGGGT 422
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTCGCCGAG 446
RESULT 10
US-10-098-732A-15
Publication 15, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 15
LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
OTHER INFORMATION: protein Mtb72F (Ra12-TbH9-Ra35 or Mtb32-Mtb39)
OTHER INFORMATION: fusion)
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(2231)
OTHER INFORMATION: Mtb72F
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)..(2287)
OTHER INFORMATION: n = g, a, c or t
US-10-098-732A-15
Alignment Scores:
Pred. No.: 1,43e-68 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-098-732A-15 (1-2287)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 63 ACAGCCGCGTCCGATTAATCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGGATC 122
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 123 GGGCAGCGGATGCGGATCGGGCCAGATCCGATCCGGTGGGGGTACCCACCGTTCTAT 182
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAnglyAenGlyAlaArg 60
Db 183 ATCGGGCTACCGCTTCCTCGCTTGGGTGGTGTTCGACAAACCGCAACGGCGCACGA 242
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCACCGGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCACGTG 302

QY 81 IleThrAlaValAlaSerGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAen 100
Db 303 ATCAGCGCGTCCAGCGCTCCGATCACTCCGCCACCGCGATGCGGACGCGCTTAAC 362
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 363 GGGCATCATCCCGTACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGCGCACGCT 422
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTGGCCGAG 446
RESULT 11
US-10-359-459-1
; Sequence 1, Application US/10359459
; Publication No. US20040013677A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE REFERENCE: 014058-009010US
; CURRENT APPLICATION NUMBER: US/10359,459
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
; OTHER INFORMATION: protein Ra12-TD9-Ra35
; NAME/KEY: modified_base
; LOCATION: (30)
; OTHER INFORMATION: n = g, a, c or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (33)
; OTHER INFORMATION: n = g, a, c or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(2231)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2270)
; OTHER INFORMATION: n = g, a, c or t
US-10-359-459-1
Alignment Scores:
Pred. No.: 1,436-68 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-359-459-1 (1-2287)
QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 63 ACAGCGCGTCCGATCACTCCAGCTGCCAGGCGGCGGAGATTCCGCATTCCGATC 122
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 123 GGGCAGGCGATGGCGATCCGGGCCAGATCCGATCGGTGGGGGGTACCCACCGCTTCAT 182
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAlaArg 60

Db 183 ATCGGCGCTACCGCTTCTCGGCTTGGGTGTTGTCGACAAACGCGACGCGCACGA 242
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 302
QY 81 IleThrAlaValAlaSerGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAen 100
Db 303 ATCAGCGCGTCCAGCGCTCCGATCACTCCGCCACCGCGATGCGGACGCGCTTAAC 362
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 363 GGGCATCATCCCGTACGTCATCTCGGTGACCTGGCAACCAAGTCGGGGCGCACGCT 422
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTGGCCGAG 446
RESULT 12
US-10-369-983-8
; Sequence 8, Application US/10369983
; Publication No. US2003023593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2451
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: MTB81F (MTB72F-DPV)
US-10-369-983-8
Alignment Scores:
Pred. No.: 1,566-68 Length: 2451
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-369-983-8 (1-2451)
QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 25 ACAGCGCGTCCGATCACTCCAGCTGCCAGGCGGCGGAGATTCCGCATTCCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGGCGATGGCGATCCGGGCCAGATCCGATCGGTGGGGGGTCAACCCACCGCTTCAT 144
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAsnGlyAlaArg 60
Db 145 ATCGGCGCTTACCGCTTCTCCGCTTGGGTGTTCGACAAACGCGACGCGCACGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 264
QY 81 IleThrAlaValAlaSerGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAen 100

Db 265 ATCCGCGGTGTCACGGCGTCCGATCAATCGCCACCGCGATGGCGGCGGCTTAAC 324
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 325 GGGCATCATCCGGTACGATCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACCGGT 384
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 13
US-10-369-983-7
; Sequence 7, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Gudarian, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: MTB83F (MTB72F-MTI)
US-10-369-983-7

Alignment Scores:
Pred. No.: 1,59e-68 Length: 2487
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-369-983-7 (1-2487)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATAAATTCAGCTGTCCAGAGGTGGCGAGGATTCGCCATTCCGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGCGATGGCGATCCGCGGCCAGATCCGATCGGTGGGGGTGACCCACCGTTTCA 144
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 145 ATCGGCGCTTACCGCTTCTCGGCTTGGGTGTTCGACAAACACGCGACCGGACGTA 204
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGGTGTGGAGAGCTCCGGCGGAGTCTCGGATCTCCACCGGACGATG 264
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCCGCGGTCCGCGCTCCGATCAATCGGCCACCGCGATGGCGGACGCGCTTAAC 324
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 325 GGGCATCATCCCGTACGATCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACCGGT 384
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 14
US-10-369-983-6
; Sequence 6, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Gudarian, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2637
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: MTB89F (MTB72F-Erd14)
US-10-369-983-6

Alignment Scores:
Pred. No.: 1,7e-68 Length: 2637
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-369-983-6 (1-2637)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATAAATTCAGCTGTCCAGAGGTGGCGAGGATTCGCCATTCCGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGCGATGGCGATCCGCGGCCAGATCCGATCGGTGGGGGTGACCCACCGTTTCA 144
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 145 ATCGGCGCTTACCGCTTCTCGGCTTGGGTGTTCGACAAACACGCGACCGGACGTA 204
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGGTGTGGAGAGCTCCGGCGGAGTCTCGGATCTCCACCGGACGATG 264
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCCGCGGTCCGCGCTCCGATCAATCGGCCACCGCGATGGCGGACGCGCTTAAC 324
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 325 GGGCATCATCCCGTACGATCATCTCGGTGACCTGGCAACCAAGTCGGGCGGACCGGT 384
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 15
US-10-098-732A-64
; Sequence 64, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Gudarian, Jeffrey

APPLICANT: Corixa Corporation
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
FILE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-012010US
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 2808
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MTB72F-MAPS
OTHER INFORMATION: (r95f) fusion construct, TB MTB72F (Ra12-TDH9-Ra35)
OTHER INFORMATION: linked to Leishmania thiol-specific antioxidant
OTHER INFORMATION: (TSA or MAPS)
US-10-098-732A-64
Alignment Scores:
Pred. No.: 1.84e-68 Length: 2808
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-098-732A-64 (1-2808)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATAACTTCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGCGCATGGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCCACCCACCGTTTCA 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAsnAsnGlyAsnGlyAlaArg 60
Db 145 ATCGGGCTACCGCTTCTTCGGTGTGGTGTGTCGACAAACGCGACGGCGACGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGCGTGGCGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCAGCGTCCAGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGTTAAC 324
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 325 GGGCATCATCCCGTGACGTCTCGTGTGACCTGGCAACCAAGTCCGGCGGCGACGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGAACGTGACATTGGCCGAG 408
RESULT 16
US-10-369-983-5
Sequence 5, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderman, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3030
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion

PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 2808
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:fusion protein
OTHER INFORMATION: R95F (MTB72F-MAPS)
US-10-369-983-5
Alignment Scores:
Pred. No.: 1.84e-68 Length: 2808
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-369-983-5 (1-2808)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATAACTTCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGCGCATGGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCCACCCACCGTTTCA 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAsnAsnGlyAsnGlyAlaArg 60
Db 145 ATCGGGCTACCGCTTCTTCGGTGTGGTGTGTCGACAAACGCGACGGCGACGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACGCGTGGCGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCAGCGTCCAGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGTTAAC 324
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 325 GGGCATCATCCCGTGACGTCTCGTGTGACCTGGCAACCAAGTCCGGCGGCGACGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGAACGTGACATTGGCCGAG 408
RESULT 17
US-10-369-983-3
Sequence 3, Application US/10369983
Publication No. US20030235593A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Guderman, Jeff
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009081US
CURRENT APPLICATION NUMBER: US/10/369,983
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/357,351
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3030
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion

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; OTHER INFORMATION: protein
US-10-369-983-3
Alignment Scores:
Pred. No.: 2,02e-68 Length: 3030
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-369-983-3 (1-3030)
QY 1 ThrAlaAlaSerAspAsnProGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 595 ACGCCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGGAGGATTCGCCATTCGATC 654
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 655 GGGCAGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGTCCACCCCGTTTCAT 714
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyAlaArg 60
Db 715 ATCGGGCTACCGCTTCTCGGCTTGGGTGTGTCGACAAACACGCGGCGACGCA 774
QY 61 ValGlnArgValValGlySerAlaProAlaAspLeuGlyIleSerThrGlyAspVal 80
Db 775 GTCCAAACCGGTGTCGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGAGTG 834
QY 81 IleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 835 ATCACCAGCGTTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGCGCTTAAC 894
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 895 GGGCATCATCCCGTGTGAGTCTCTCGGTGACCTCGGTGACCTGGCAACCAAGTCGGCGGCGCGT 954
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 955 ACAGGGAACGTGACATTGGCCGAG 978

RESULT 18
US-10-369-983-11
; Sequence 11, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderman, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 3060
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fusion protein
; OTHER INFORMATION: MTB103F (MTB72F-85b)
US-10-369-983-11
Alignment Scores:
Pred. No.: 2,04e-68 Length: 3060
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

US-09-684-215B-23 (1-128) x US-10-369-983-11 (1-3060)
QY 1 ThrAlaAlaSerAspAsnProGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGCCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGGAGGATTCGCCATTCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGTCCACCCCGTTTCAT 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAspAsnAsnGlyAlaArg 60
Db 145 ATCGGGCTACCGCTTCTCGGCTTGGGTGTGTCGACAAACACGCGGCGACGCA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAspLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCAAACCGGTGTCGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGAGTG 264
QY 81 IleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCAGCGTTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGCGCTTAAC 324
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 325 GGGCATCATCCCGTGTGAGTCTCTCGGTGACCTCGGTGACCTGGCAACCAAGTCGGCGGCGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 19
US-10-369-983-10
; Sequence 10, Application US/10369983
; Publication No. US20030235593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderman, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3104
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fusion protein
; OTHER INFORMATION: MTB102tm2F (MTB72F-HTCC#1)
US-10-369-983-10
Alignment Scores:
Pred. No.: 2,08e-68 Length: 3104
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-369-983-10 (1-3104)
QY 1 ThrAlaAlaSerAspAsnProGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGCCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGGAGGATTCGCCATTCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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Db 85 GGCACGGGATGCGATCGCGGCCAGATCCGATCGGTTGGGGGTCAACCCACCGTTCTAT 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArg 60
Db 145 ATCGGCGCTACCGCTTCTCTCGCTTGGTGTTCGACACAAACGCAACGGCGCAGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyTleSerThrGlyAspVal 80
Db 205 GTCCAAACGGGTGTCGGGAGCGTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGCTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCAGCGCGGTTCAGCGGCTCCGATCACTCGGCCACCGCGATGCGGACGCGCTTAAC 324
QY 101 GlyHisProGlyAspValIleSerValThrTirpGlnThrIlysserGlyGlyThrArg 120
Db 325 GGCATCATCCCGGTGACGTCATCTCGTGACCTTGGCAACCAAGTCCGGCGGACGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408
RESULT 20
US-10-369-983-9
; Sequence 9, Application US/10369983
; Publication No. US2003023593A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3474
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: MTB114F (MTB72F-mtCCH2)
US-10-369-983-9
Alignment Scores:
Pred. No.: 2 39e-68 Length: 3474
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-09-684-215B-23 (1-128) x US-10-369-983-9 (1-3474)
QY 1 ThrAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGGCTCCGATACTTCAGCTGTCACAGGTCGGCGGAGTTCGCCATTCCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 85 GGGCAGGCGATGGCGATCCGGCGGCGAGATCCGATCGGTTGGGGGTCAACCCACGTTTCAT 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArg 60
Db 145 ATCGGCGCTACCGCTTCTCTCGCTTGGTGTTCGACACAAACGCAACGGCGCAGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyTleSerThrGlyAspVal 80

Db 205 GTCCAAACGGGTGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGCTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCAGCGCGGTTCAGCGGCTCCGATCACTCGGCCACCGCGATGCGGACGCGCTTAAC 324
QY 101 GlyHisProGlyAspValIleSerValThrTirpGlnThrIlysserGlyGlyThrArg 120
Db 325 GGCATCATCCCGGTGACGTCATCTCGTGACCTTGGCAACCAAGTCCGGCGGACGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408
RESULT 21
US-10-193-002-4
; Sequence 4, Application US/10193002
; Publication No. US20030135028A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/193,002
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-193-002-4
Alignment Scores:
Pred. No.: 7 87e-69 Length: 447
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 15 Gaps: 0

TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-084-843-4
Alignment Scores: 7.87e-69 Length: 447
Pred. No.: 646.00 Matches: 127
Score: 99.22% Conservative: 0
Percent Similarity: 99.22% Mismatches: 1
Best Local Similarity: 99.22% Indels: 0
Query Match: 99.23% Gaps: 0
DB: 15
US-09-684-215B-23 (1-128) x US-10-084-843-4 (1-447)
QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGGCTCCGATTAATTCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGGCGATGGCGATCCGGGCGAGATCCGATCGGCTGGGGTCCACCCACCGTTTCAT 130
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60
Db 131 ATCCGCGCTACCGCTTCTCGGCTTGGTGTTCGCAACAACGCGACGCGACGCA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 250
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCCACCGGCTCGACGGCGCTCCGATCAACTCGGCGACCGCGATGGCGGACGCTTAAC 310
QY 101 GlyHisHisProGlyAspValIleSerValThrTyrGlnThrIleSerGlyGlyThrArg 120
Db 311 GGGCATCATCCCGGTGACGTCTCGGTGAACCTCGGTGAACCTCGGTGAACCTCGGTGAACCTCGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 371 ACAGGGAACGTGACATTGGCCGAG 394
RESULT 23
US-10-098-732A-9
; Sequence 9, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Guderian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Leishmania Antigen
; FILE REFERENCE: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MTBRa12 (MTB32A
; OTHER INFORMATION: C-terminus)

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US-10-098-732A-9
Alignment Scores:
Pred. No.: 7,87e-69 Length: 447
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-098-732A-9 (1-447)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGCGTCCGATAAATCCAGCTGTCCAGGTTGGCGAGGATTCGCCATTCCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 71 GGGCAGCGATGGCGATCCGCGCCAGATCCGATCGGGTGGGGGTCCACCCACCGTTTCA 130
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 131 ATCGGCGCTACCGCTTCTTCGGCTGGGTGGTGTTCGACAAACAGCGCACGGCGACGA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACAGCGTGGTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 250
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCCACCGCGTCCAGCGCTCCGATCACTCGGCACCGCATGGCGGACGGCTTTAAC 310
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 311 GGGCATCATCCCGTGCAGCTCATCTCGTGAATCGCAACCAAGTCCGGCGGCGACGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 371 ACAGGAAACGTGACATTGGCCGAG 394

RESULT 24
US-10-193-002-17
; Sequence 17, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedvick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/193,002
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-193-002-17
Alignment Scores:
Pred. No.: 4.5e-68 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-193-002-17 (1-1872)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACGGCGCGTCCGATAAATCCAGCTGTCCAGGTTGGCGAGGATTCGCCATTCCGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 818 GGGCAGCGATGGCGATCCGCGGCAATCCGATCGGGTGGGGGTCCACCCACCGTTTCA 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 878 ATCGGCGCTACCGCTTCTTCGGCTGGGTGGTGTTCGACAAACAGCGCACGGCGACGA 937
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 938 GTCCACAGCGTGGTCCGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCCACCGCGTCCAGCGCTCCGATCACTCGGCACCGCATGGCGGACGGCTTTAAC 1057
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGTGCAGCTCATCTCGTGAATCGCAACCAAGTCCGGCGGCGACGGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 1118 ACAGGAAACGTGACATTGGCCGAG 1141

RESULT 25
US-10-084-843-17
; Sequence 17, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; Skeiky, Yasir A.W.
; Dillon, Davin C.
; Campos-Neto, Antonio
; Houghton, Raymond
; Vedvick, Thomas S.
; Twardzik, Daniel R.
; Lodes, Michael J.
; Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; AND DIAGNOSIS OF TUBERCULOSIS
```

NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/084,843
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-084-843-17

Alignment Scores:
Pred. No.: 4.5e-68 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-084-843-17 (1-1872)

Qy	1	ThrAlaAlaSerAspAsnProGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle	20
Db	758	ACGGCGCGTCCGATTAATCCAGCTGTCACGGTGGCGAGGATTCCGCAATCCGATC	817
Qy	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis	40
Db	818	GGGCGAGCGGATGGCGATCGCGGCCAAATCCGATCGGGTGGGGGTCAACCCCGTTTCAT	877
Qy	41	IleGlyProThrAlaPheLeuGlyValValAspAsnGlyAsnGlyAlaArg	60
Db	878	ATCGGGCTACCGCTTCCTCGGCTTGGGTGGTTCGACAAACGCGACGCGACGA	937
Qy	61	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	80
Db	938	GTCCAAACGCGTGGTGGGAAGCGTCCGCGCGCAAGTCTCGGCATCTCCACCGCGCGGTG	997
Qy	81	IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn	100
Db	998	ATCACCGGCTACGCGCTCCGATCAATCGGCCACCGGATGGGGAGCGGCTTAAC	1057
Qy	101	GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyThrArg	120
Db	1058	GGGCATCATCCCGTACGTCATCTCGTGAACCTGGCAACCAAGTCGGCGCGCGCGT	1117
Qy	121	ThrGlyAsnValThrLeuAlaGlu	128
Db	1118	ACAGGGAACGTGACATTGGCCGAG	1141

RESULT 27
US-09-759-143-822
; Sequence 822, Application US/09759143
; Patent No. US2002002248A1

RESULT 26
US-10-098-732A-1
; Sequence 1, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Guderian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Leishmania Antigen
; FILE OF INVENTION: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: MTB32A (Ra35FL)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(1872)
; OTHER INFORMATION: n = g, a, c or t
US-10-098-732A-1

Alignment Scores:
Pred. No.: 4.5e-68 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-23 (1-128) x US-10-098-732A-1 (1-1872)

Qy	1	ThrAlaAlaSerAspAsnProGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle	20
Db	758	ACGGCGCGTCCGATTAATCCAGCTGTCACGGTGGCGAGGATTCCGCAATCCGATC	817
Qy	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis	40
Db	818	GGGCGAGCGGATGGCGATCGCGGCCAAATCCGATCGGGTGGGGGTCAACCCCGTTTCAT	877
Qy	41	IleGlyProThrAlaPheLeuGlyValValAspAsnGlyAsnGlyAlaArg	60
Db	878	ATCGGGCTACCGCTTCCTCGGCTTGGGTGGTTCGACAAACGCGACGCGACGA	937
Qy	61	ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal	80
Db	938	GTCCAAACGCGTGGTGGGAAGCGTCCGCGCGCAAGTCTCGGCATCTCCACCGCGCGGTG	997
Qy	81	IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn	100
Db	998	ATCACCGGCTACGCGCTCCGATCAATCGGCCACCGGATGGGGAGCGGCTTAAC	1057
Qy	101	GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyThrArg	120
Db	1058	GGGCATCATCCCGTACGTCATCTCGTGAACCTGGCAACCAAGTCGGCGCGCGCGT	1117
Qy	121	ThrGlyAsnValThrLeuAlaGlu	128
Db	1118	ACAGGGAACGTGACATTGGCCGAG	1141

RESULT 27
US-09-759-143-822
; Sequence 822, Application US/09759143
; Patent No. US2002002248A1

GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-822

Alignment Scores:
Pred. No.: 4,97e-64 Length: 675
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 4
Query Match: 93.39% Indels: 4
DB: 9 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-759-143-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAlaAsnAsnGlyValAlaArg 60
Db 130 ATCGGGCTACCGCTTCTCGGTTGGGTGTTCGACAAACACGCGACGCGACGA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyTieserThrGlyAspVal 80
Db 190 GTCCACGCGTGGTCCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGACGTG 249
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATACCGCGGTGACGCGCTCCGATCACTCCGCCACCGCATGGCGAGCGCGTTTAC 309
QY 101 GlyHisProGlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArg 120
Db 310 GGGCATCATCCCGTACGTCATCTCGTACCTGGCAACCAAGTCCGGCGCGCGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 370 ACAGGAAACGTGACATTGGCGGAG 393

RESULT 28
US-09-780-669-822
; Sequence 822, Application US/09780669
; Patent No. US2002005197A1

GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-822

Alignment Scores:
Pred. No.: 4,97e-64 Length: 675
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 4
Query Match: 93.39% Indels: 4
DB: 9 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-780-669-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAlaAsnAsnGlyValAlaArg 60
Db 130 ATCGGGCTACCGCTTCTCGGTTGGGTGTTCGACAAACACGCGACGCGACGA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyTieserThrGlyAspVal 80
Db 190 GTCCACGCGTGGTCCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGACGTG 249
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATACCGCGGTGACGCGCTCCGATCACTCCGCCACCGCATGGCGAGCGCGTTTAC 309
QY 101 GlyHisProGlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArg 120
Db 310 GGGCATCATCCCGTACGTCATCTCGTACCTGGCAACCAAGTCCGGCGCGCGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 370 ACAGGAAACGTGACATTGGCGGAG 393

RESULT 29

```
US-09-822-827-822
; Sequence 822, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-827-822

Alignment Scores:
Pred. No.: 4,97e-64 Length: 675
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.39% Indels: 4
DB: 9 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-822-827-822 (1-675)
Qy 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCCGCGTCCGATTAATTCACAGTGTCCAGGGTGGGACGGATTCGCCATTCGCATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGCGCATGGCATCGCGGGCGAGATCAAG-----CTTCCACCGTTTCAT 129
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAenGlyValAsnGlyValAsn 60
Db 190 GTCCAACGCGTGTGCGGAGCGCTCCGCGGCAAGTCTCGCATCTCCACCGCGACGTG 249
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACC CGGTCGACGCGCTCCGATCAATCGGCGCACCGCGATGGCGGACGCTTAAC 309
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyThrArg 120
Db 310 GGGCATCATCCGCTGACGTGACGTATCTCGGTGACCTGGCAACCAAGTGGCGGACGCGT 369

RESULT 30
US-09-895-793-822
; Sequence 822, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Baasols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-793-822

Alignment Scores:
Pred. No.: 4,97e-64 Length: 675
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.39% Indels: 4
DB: 9 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-895-793-822 (1-675)
Qy 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCCGCGTCCGATTAATTCACAGTGTCCAGGGTGGGACGGATTCGCCATTCGCATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGCGCATGGCATCGCGGGCGAGATCAAG-----CTTCCACCGTTTCAT 129
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAenGlyValAsnGlyValAsn 60
Db 130 ATCCGCGCTACCGCTTCTCGGTGGGTGTGTGACAAACACGCAACGGCGCACGA 189
Qy 61 ValGlnArgValValGlySerAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 80
Db 190 GTCCAACGCGTGTGCGGAGCGCTCCGCGGCAAGTCTCGCATCTCCACCGCGACGTG 249
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACC CGGTCGACGCGCTCCGATCAATCGGCGCACCGCGATGGCGGACGCTTAAC 309
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyThrArg 120
Db 310 GGGCATCATCCGCTGACGTGACGTATCTCGGTGACCTGGCAACCAAGTGGCGGACGCGT 369

Search completed: April 30, 2004, 05:10:29
Job time : 474.379 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 22:25:27 ; Search time 2507.02 Seconds
(without alignments)
1524.860 Million cell updates/sec

Title: US-09-684-2158-23
Perfect score: 651
Sequence: 1 TAASDNFQLSQGGQFAIPI.....SVTWTKSGGRTGNTGNVLAE 128

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO.spool/US09684215/runat_29042004_061305_13200/app.query.fasta_1.1180
-DB=EST -OPMT=fastap -SUPX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09684215@cgn2.1 1.5167 @runat_29042004_061305_13200 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: em_estba:*
2: em_estba:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_pro:*
26: em_gss_rod:*
27: em_gss_plg:*
28: em_gss_vrl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	145.5	22.4	289	29	U82114	U82114 U82114 orde
C 2	126.5	19.4	1438	28	BH770798	BH770798 LLMtag54
C 3	122	18.7	959	28	BZ549048	BZ549048 pacb1-60
C 4	120.5	18.5	726	14	CB679186	CB679186 OSJNEf02F
C 5	117.5	18.0	590	14	CB925602	CB925602 ABAL 22_F
C 6	115.5	17.7	807	14	CA228900	CA228900 SCQFL305
C 7	114	17.5	603	28	AZ934428	AZ934428 BJ_Ba000
C 8	113	17.4	758	13	BQ514888	BQ514888 EST22303
C 9	108	16.6	982	14	CD080132	CD080132 MA3-9999U
C 10	106.5	16.4	1033	28	BZ561390	BZ561390 pac82-164
C 11	103.5	15.9	947	28	BZ549047	BZ549047 pacb1-60
C 12	103	15.8	726	28	AQ989479	AQ989479 Rfc00025-
C 13	102	15.7	719	28	AZ933900	AZ933900 BJ_Ba000
C 14	102	15.7	785	9	AJ558965	AJ558965 AJ558965
C 15	100.5	15.4	859	14	CA480614	CA480614 AGENCOURT
C 16	99	15.2	423	9	AI597611	AI597611 tnl5f02.x
C 17	97.5	15.0	499	12	BI350520	BI350520 fr32b05.Y
C 18	97.5	15.0	870	14	CA473840	CA473840 AGENCOURT
C 19	97	14.9	444	13	CA148171	CA148171 SCEZR2101
C 20	97	14.9	543	12	BI721127	BI721127 103105481
C 21	96	14.7	546	10	AW285510	AW285510 LGL_241_E
C 22	96	14.7	551	10	AW285527	AW285527 LGL_241_G
C 23	95.5	14.7	677	12	BI378928	BI378928 BFLGI_000
C 24	95	14.6	909	14	CA375497	CA375497 AGENCOURT
C 25	94.5	14.5	600	14	CF787130	CF787130 854999_MA
C 26	94.5	14.5	647	13	BX674871	BX674871 BX674871
C 27	94.5	14.5	728	12	RJ285991	RJ285991 BJ285991
C 28	93.5	14.4	600	28	CC345457	CC345457 CQCAR70TH
C 29	93.5	14.4	907	14	CA471201	CA471201 AGENCOURT
C 30	93.5	14.4	913	14	CF265501	CF265501 AGENCOURT
C 31	93	14.3	951	14	CA474469	CA474469 AGENCOURT
C 32	92.5	14.2	709	29	CG935905	CG935905 pastbac00
C 33	92.5	14.2	860	14	CA471291	CA471291 AGENCOURT
C 34	92.5	14.2	949	14	CF243195	CF243195 AGENCOURT
C 35	92.5	14.2	1394	28	BZ576076	BZ576076 mah2_4761
C 36	92	14.1	766	14	CF997044	CF997044 AGENCOURT
C 37	92	14.1	790	14	CK127722	CK127722 AGENCOURT
C 38	92	14.1	894	28	BZ578796	BZ578796 mah2_6009
C 39	92	14.1	899	14	CA471516	CA471516 AGENCOURT
C 40	91.5	14.1	452	12	BM874057	BM874057 laa07a02.
C 41	91.5	14.1	513	12	BM036648	BM036648 fu80g01.Y
C 42	91.5	14.1	555	13	BQ479512	BQ479512 faa68g09
C 43	91.5	14.1	570	14	CB364397	CB364397 EF001.P00
C 44	91.5	14.1	613	10	AW595047	AW595047 FX28603.Y
C 45	91.5	14.1	631	14	CF512107	CF512107 CABud0004

ALIGNMENTS

RESULT 1
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LOCUS U82114 ordered cosmid library Mycobacterium leprae genomic clone
DEFINITION cosmid L-373; contig 64, genomic survey sequence.
ACCESSION U82114
VERSION U82114.1 GI:3647212
KEYWORDS GSS.
SOURCE Mycobacterium leprae
ORGANISM Mycobacterium leprae
Bacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 289)

Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
source
1. 959
/organism="Pseudomonas aeruginosa"
/mol_type="Genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacs1-60.1644"
/clone_lib="pacs1-60"
/note="clinical isolate 1-60 whole genomic shotgun
library."

ORIGIN
Alignment Scores:
Pred. No.: 0.0809 Length: 959
Score: 122.00 Matches: 40
Percent Similarity: 47.29% Conservative: 21
Best Local Similarity: 31.01% Mismatches: 44
Query Match: 18.74% Indels: 24
DB: 28 Gaps: 5

US-09-684-215B-23 (1-128) x BZ549048 (1-959)

QY 4 SerAspAspPheGlnLeuSerGlnGly-----GlyGlnGlyPheAlaIleProIleGly 21
DB 378 TGCAGATCTTACCCGTTCCGGCGCTCATCGGCGCTGCTTCGCCATTCGATCCAT 319
QY 22 GlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle 41
DB 318 GTCGGCGTGAAGCTGCCGCCACCATGTTGAAGAAAGCGGC-----AAGGTCACTGCGC 268
QY 42 GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAen----- 55
DB 267 GGC-----TGGCTGGCGTGTGATCCAGAGTGAACAAGATCTCCCGAGTCC 217
QY 56 -----GlyAsnGlyAlaArgValGlnArgValValGlySerAlaProIla 70
DB 216 TACGGCTCGACAGCGCTCCGGCGCTGTGGCGCAACTGTTGAAGAGCGCCGCGC 157
QY 71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsn 90
DB 156 GCCAAGGTGGCTCGAGTGGCGCATGTGATCATAAGCTTGAACGCCGACGTCGATCAAC 97
QY 91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
DB 96 GAGTCGCCGCACTGCGCACCTGGTGGCGCAACATGACATGAACCGCGGACAGATCAACCTG 37
QY 111 ThrTrpGlnThrLysSerGlyThr 119
DB 36 -----GACGGGGGATCC 25

RESULT 4
CB679186/c 726 bp mRNA linear EST 09-APR-2003
LOCUS
DEFINITION
OSJNEF02F19.r OSJNEF Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEF02F19 3', mRNA sequence.
CB679186
ACCESSION
VERSION
CB679186.1 GI:29682911
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 726)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,B.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: F column: 19
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers

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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEF02F19"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEF"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

FEATURES
source
Alignment Scores:
Pred. No.: 0.0761 Length: 726
Score: 120.50 Matches: 41
Percent Similarity: 44.03% Conservative: 18
Best Local Similarity: 30.60% Mismatches: 50
Query Match: 18.51% Indels: 25
DB: 14 Gaps: 4

US-09-684-215B-23 (1-128) x CB679186 (1-726)
QY 10 SerGlnGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAla----- 27
DB 579 ACATCTGCTGGTGTGTTTGGCATCCGTCATCAACTGTTCTGAAATAGCTCCTCAG 520
QY 28 -----GlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro 43
DB 519 TTAATTCAGTTTGAAGAAGTTCGCCGTGGCTTGAATGGAGTTGCTCCAGATCCA 460
QY 44 ThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg 63
DB 459 ATCGCATAT-----CAGCTTAATGTTGGCACTGGATCTATAATATTCAG 415
QY 64 ValValGlySerAlaProAlaAlaSerLeuGly----- 74
DB 414 GTTCCTGGGGCGCATGCTGCAGCCAAAGCTGGTCTGTTCTACCATAGGGGTTTGTCT 355
QY 75 -----IleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAla 92
DB 354 GGTACCATTTCTTGTGTGATGTCATTGTTGCCGTGGACGGTAACCTATCAAAGGCAAA 295
QY 93 ThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112
DB 294 TCTGATCTATCAGGGGTTCTGGATGCTTATGGCGTTGAGACCAAGGTGAGCTTGACAATC 235
QY 113 GlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 126
DB 234 CAAGA-----GGCGCTGATCTCTGGAGGTAACTTGT 202

```
RESULT 5
CB925602
LOCUS
DEFINITION
ABAI_22_F06.b1_A012 Abscisic acid-treated seedlings Sorghum bicolor
CDNA clone ABAI_22_F06_A012 3', mRNA sequence.
ACCESSION
CB925602
VERSION
CB925602.1 GI:30161873
KEYWORDS
EST
SOURCE
Sorghum bicolor (sorghum)
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 590)
Cordonnier-Pratt M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
Klein, R., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D.,
Easman, A. and Pratt, L.H.
An EST database from Sorghum: ABAI-treated seedlings
Other ESTs: ABAI_22_F06.g1_A012
Unpublished (2003)
Contact: Cordonnier-Pratt NM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3 (CGACCTGCAGCTCGAGCAC)
POLYA=Yes.
FEATURES
Location/Qualifiers
1..590
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="IS3620C"
/db_xref="taxon:4558"
/clone="ABAI_22_F06_A012"
/lab_host="DH10B-T1 phage-resistant E. coli"
/notes="Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. After 12 days, medium was
supplemented with 1 mM abscisic acid (ABA), while leaves
were misted with a solution of 1 mM ABA. Roots and leaves
were harvested after 3, 6, 12, and 24 hr and material from
all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."
ORIGIN
Alignment Scores:
Pred. No.: 0.112 Length: 590
Score: 117.50 Matches: 37
Percent Similarity: 44.19% Conservative: 20
Best Local Similarity: 28.68% Mismatches: 43
Query Match: 18.05% Indels: 29
DB: 14 Gaps: 4
US-09-684-215B-23 (1-128) x CB925602 (1-590)
Gly 28
15 GlyPheAlaIleProIleGlyGlnAlaMetAlaIleAala-----Gly 28
:::
6 GCGTTTGCTATTCATCATCACTGTACTTAAATCGCTCTCAGTTAATTCAGTTCGGA 65
```

```
QY 29 GlnIleArgSerGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGly 48
:::
Db 66 AAGATTTCGTCGTCGCTGGCTTGAATGGACATTCGCTCCGATCCCAATTCATAT----- 119
:::
QY 49 LeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAla 68
:::
Db 120 -----CAGCTTAATGTTCCACGAGGAGCTCTTATATCTTAAGGTACCTGGGGGCGAGT 170
:::
QY 69 ProAlaIleSerLeuGlyIleSer-----Thr 77
:::
Db 171 GCTGCAAGCCAAACGAGCTTGTCTCAACCGGCGAGGGTTTGTCTGTAATATTGTTCTG 230
:::
QY 78 GlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsp 97
:::
Db 231 GGTGATATCATCTGTCAGTGGACGCAAACTGTTAAGGCGCAAAATCTGACCTGCTGAGG 290
:::
QY 98 AlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTIpGlnThrIlysserGly 117
:::
Db 291 GTTCTGATGACTATGCGTCGAGATCAGGTGACCTTGACA----- 332
:::
QY 118 GlyThrArgThrGlyAsnValThrLeu 126
:::
Db 333 ---ATCCGGCGAGGCTCAGAAACCCCTT 356
:::
RESULT 6
CA228900/c
LOCUS
DEFINITION
CA228900 807 bp mRNA linear EST 25-SEP-2003
CDNA clone SCQGLF3058G06 5', mRNA sequence.
ACCESSION
CA228900
VERSION
CA228900.1 GI:35290878
KEYWORDS
EST
SOURCE
Saccharum officinarum
ORGANISM
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE
1 (bases 1 to 807)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: Clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 058 row: G column: 06
Seq primer: T7 Promoter Primer.
FEATURES
Location/Qualifiers
1..807
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCQGLF3058G06"
/lab_host="DH10B"
/notes="Organ: Base of developing inflorescence (5cm-long);
Vector: pSPort1; Site_1: SalI; Site_2: NotI; An
unidirectional cDNA library generated from (base of
developing inflorescence (5cm-long)). cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
```

```

/strain="USDAL110"
/db_xref="taxon:375"
/lab_host="E. coli"
/clone_lib="B. japonicum BAC library"
/note="vector: pindigo536; Site_1: HindIII"

ORIGIN

Alignment Scores:
Pred. No.: 0.257 Length: 603
Score: 114.00 Matches: 36
Percent Similarity: 43.44% Conservative: 17
Best Local Similarity: 29.51% Mismatches: 57
Query Match: 17.51% Indels: 12
DB: 28 Gaps: 4

US-09-684-215B-23 (1-128) x AZ934428 (1-603)

QY 13 GlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer 32
Db 245 GCATCGGTTTCATCCCGCCACACCGTGAAGCGTGTGTGCCAGTCAAGAC 304
QY 33 GlyGly-----GlySerProThrValHisIleGlyProThrAlaPheLeuGly 48
Db 305 AAGGGTTCGTCAGCGCGGCTGGATCGCGTTCAGATTCAAGCGGTGACG----- 355
QY 49 LeuGlyValValAspAsnAsnGly-----AsnGlyAlaArgValGlnArgVal 64
Db 356 TCGATATCCCGACAGCTCGGCATGAAGAGCCGAGGGGCGTGTGCGGAGCGC 415
QY 65 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 84
Db 416 CAGGCGCAAGCGTCCGCGCGGCGAAGCGCGGCATCGAGTCCGCGGACGTGATCACCCTCGTC 475
QY 85 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 104
Db 476 AACGGGATCGTCAAGGACGCGCGAGTCTGCGCCGACCATCGCGGCGCATGCGGCGCC 535
QY 105 GlyAspValIleSerValThrTrpGlnThrIlysserGlyGlyThrArgThrGlyAsnVal 124
Db 536 CGTGCATCGTGAAGCTTAACGTGTGCACAAG---GGCCAGGACAATGTCTGAACCTC 592

QY 125 ThrLeu 126
Db 593 ACCCTC 598

RESULT 8
BQ514888/c
LOCUS
DEFINITION
BQ514888 758 bp mRNA linear EST 07-MAR-2003
Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STM1081
3' end, mRNA sequence.
ACCESSION
VERSION BQ514888.1 GI:21373757
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 758)
Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
Other ESTs: EST622302
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

```

tosoma

SP,

EST
nd
seen

-- 23

AA 414

LS 40

CA 474

-- 44

CT 534

al 51

::

IA 594

al 65

::

IA 654

sp 85

||

AT 714

EC-2002
lone

pacs2-164_3239, genomic survey sequence.
 BZ561390
 DEFINITION BZ561390.1 GI:27181349
 GSS.
 Pseudomonas aeruginosa
 Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 1 (bases 1 to 1033)
 Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
 Burns, J.L., Kaul, R. and Olsen, M.V.
 Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol. (2002) In press
 Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: shotgun.
 Location/Qualifiers
 source
 1..1033
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="2-164"
 /db_xref="taxon:287"
 /clone="pacs2-164_3239"
 /clone_lib="pacs2-164"
 /note="clinical isolate 2-164 Whole genomic shotgun
 library."

ORIGIN

Alignment Scores:
 Pred. No.: 3.11 Length: 1033
 Score: 106.50 Matches: 41
 Percent Similarity: 44.20% Conservative: 20
 Best Local Similarity: 29.71% Mismatches: 56
 Query Match: 16.36% Indels: 21
 DB: 28 Gaps: 4
 US-09-684-215B-23 (1-128) x BZ561390 (1-1033)

QY 4 SerAspAsnPhcInLeuSerGInGlyGln-----GlyPheAlaIleProIleGly 21
 DB 713 TCCAGTATTTCCACCGGTCGCGGCTCAATGCCCTCTTTTCGGCATTCCGATCGAT 654
 QY 22 GlnAlaMetAlaIle-AlaGlyGlnIleArg-----Se 32
 DB 653 GTCGGGTGACCTTCGCGACCAAGTGAAGAAAGCCGCAAGGTCAAGTCGGGTGGC 594
 QY 32 rGlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeu-GlyLeuGlyValV 52
 DB 593 TGGCGGTGGTGTATCCAGGAAGTGAACCAAGATCTCCCGAGTCCTTCGGCCTC----- 541
 QY 52 alAspAsnGlyAsnGlyValAlaArgValGlnArgValGlySerAlaProAlaAlas 72
 DB 540 -----GACAAGCCGTCGCGGCGCTGGTGGCGCACTGGTGGAGACGCGCGCGCCA 486
 QY 72 erLeuGlyIleSerThrGlyAspValIleThrAlaValaspGlyAlaProIleAsnSerA 92
 DB 485 AGGGTGGCCTTCGAGGTGGGGGATGTGATCTCAGCTGAACGCCAGTCATCAACGAT 426
 QY 92 laThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal---- 110
 DB 425 CCGCGGACCTTGGCCACTGGTGGGCAACATGAGCGGGCGCACAGATCAACTGGACG 366
 QY 111 -----ThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 124
 DB 365 TGATTGCAACGGCCAGCGCAAGTCCCTGAGCATGGCGGTAGCAGCCTT 316

RESULT 11

BZ549047/c
 LOCUS
 DEFINITION BZ549047 947 bp DNA linear GSS 17-DEC-2002
 pacs1-60_1644.s1 pacs1-60 Pseudomonas aeruginosa genomic clone
 BZ549047
 GSS.
 Pseudomonas aeruginosa
 Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 1 (bases 1 to 947)
 Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
 Burns, J.L., Kaul, R. and Olsen, M.V.
 Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol. (2002) In press
 Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: shotgun.
 Location/Qualifiers
 source
 1..947
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="1-60"
 /db_xref="taxon:287"
 /clone="pacs1-60_1644"
 /clone_lib="pacs1-60"
 /note="clinical isolate 1-60 Whole genomic shotgun
 library."

ORIGIN

Alignment Scores:
 Pred. No.: 5.43 Length: 947
 Score: 103.50 Matches: 37
 Percent Similarity: 44.74% Conservative: 14
 Best Local Similarity: 32.46% Mismatches: 48
 Query Match: 15.90% Indels: 16
 DB: 28 Gaps: 3
 US-09-684-215B-23 (1-128) x BZ549047 (1-947)
 QY 4 SerAspAsnPhcInLeuSerGInGly-----GlyGlnGlyPheAlaIleProIleGly 21
 DB 374 TCGCAGATCTTCACTCCCGGCTTCATGGCGCTTCCTTCGCCATTCGATCGAT 315
 QY 22 GlnAlaMetAlaIleAlaGlyGlnIleArgSer----- 32
 DB 314 GTCGGATGAACGTGCGCGACCACTTGAAGAAAGCCGCAAGGTCACTCGCGGTGGTG 255
 QY 33 GlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGlyValVal 52
 DB 254 GCGGT-GGTGATCCAGGAAGTGAACAACGATCTCCCGAGTCTTCGGCCTC----- 205
 QY 53 AspAsnGlyAsnGlyValAlaArgValGlnArgValGlySerAlaProAlaAlaSer 72
 DB 204 ---GACAAGCCGTCGCGGCGCTGGTGGCGCACTGGTGGAGACGCGCGCGCGAAG 148
 QY 73 LeuGlyIleSerThrGlyAspValIleThrAlaValaspGlyAlaProIleAsnSerAla 92
 DB 147 GGTGGCCTTCAGGTGGGGATGTGATCAACAGCCTGAACGCCAGTCATCAACGATCC 88
 QY 93 ThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAsp 106
 DB 87 GCGGACCTTGGCGCACTGGTGTGGAAACATGAGCGGGCGGAC 46
 RESULT 12
 AQ989479

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

AQ989479 726 bp DNA linear GSS 14-AUG-2000
Rf000025 Photorhabdus luminescens strain W14 M13 library genomic survey sequence.
Photorhabdus luminescens genomic clone PLG00025, genomic survey sequence.
AQ989479
AQ989479.1 GI:9648073
GSS.
Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 726)
ffrench-Constant R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D., and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
10919786
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bserf@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .726
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00025"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

FEATURES
source
1. .726
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00025"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN
Alignment Scores:
Pred. No.: 4.14 Length: 726
Score: 103.00 Matches: 39
Percent Similarity: 46.55% Conservative: 15
Best Local Similarity: 33.62% Mismatches: 52
Query Match: 15.82% Indels: 11
DB: 28 Gaps: 2

US-09-684-215B-23 (1-128) x AQ989479 (1-726)

QY 6 AsnProGlnLeuSerGlnGlyGln-----GlyPheAlaIleProIle 20
Db 179 TCATTCGATAAAGTGAATGGTGAACCCAGAGGGTGGGTTTCGTATCCGACT 238
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 239 GAATCGCTACTAAGATTATGCGAAGACTTATCCGTGACGACGAGTTATCCGGGTTTT 298
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsn----- 57
Db 299 ATCGGCATACATCGCAAGAGTCCACATATTCGCTCTTCTAACGGCAATATTACACG 358
QY 58 -----GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIle 75
Db 359 CTTCAAGGGCTACGAGTATTTACAGTAACATAACACCGGCTCGCAAAAAGCCGGTATT 418
QY 76 SerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMet 95

Db 419 AAAGTGGGTGATCATCATACCGCTCAATAACAAACCGCTATTTCGCGGTGAACA 478
QY 96 AlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThr 111
Db 479 ATGATCAAGTGCTGA-AATACCCCGCAGCGGGTCTGTCTACT 525

RESULT 13
AZ933900 719 bp DNA linear GSS 24-APR-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BJ_Ba0001B03r B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence.
AZ933900
AZ933900.1 GI:13775960
GSS.
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.
1 (bases 1 to 719)
Tomkins, J.P., Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A., Goicoechea, J.L., Stacey, G., Sadowsky, M.J., and Wing, R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum genome
Genome Res. 11 (8), 1434-1440 (2001)
21376150
11483585
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 671.
Location/Qualifiers
1. .719
/organism="Bradyrhizobium japonicum"
/mol_type="genomic DNA"
/strain="USDAL10"
/db_xref="taxon:375"
/lab_hosts="E. coli"
/clone_lib="B. japonicum BAC library"
/notes="Vector: pIndigoS36; Site_1: HindIII"

ORIGIN
Alignment Scores:
Pred. No.: 5.13 Length: 719
Score: 102.00 Matches: 26
Percent Similarity: 44.44% Conservative: 14
Best Local Similarity: 28.89% Mismatches: 40
Query Match: 15.67% Indels: 10
DB: 28 Gaps: 2

US-09-684-215B-23 (1-128) x AZ933900 (1-719)

QY 13 GlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer 32
Db 44 GGCATCGGCTTTGGCATCTTGTCAATCGAGCGCTGCTCGCTCCGCCAAGGGC 103
QY 33 GlyGly-----GlySerProThrValHisIleGlyProThr 44
Db 104 GCGCGCAAGCGGTGAACGTCCTCGCTGGCGCGGAGTTGCGAGCGGTGACGCCGAG 163
QY 45 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 64
Db 164 ATCGCCGAAGACCTCGGCTTG-----CGTTCGCGCAGCGCGGCTGTCGCGAGGGTG 217
QY 65 ValGlySerAlaProAlaAlaSerIleGlySerThrGlyAspValIleThrAlaVal 84
Db 218 GTCTCGAACGTCGCGCAGCGGCTGAAATCTCTCCGATCTGATCCCGGATC 277


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Db      572  GTAGATGGGCACAGTGTGGGTGACACCATACACAGAGTCCATCATCAGATACCAGTGGTAGC 513
Qy      119  ThrArg-----ThrGlyAsnVal 124
Db      512  ACCAGGAGATACAGGACAGCACAGCCTGGATGGCAACGTA 471

RESULT 16
Al597611
LOCUS   Al597611
DEFINITION   nt15f02.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167707 3' similar to TR:O08664 O08664 BCL7C MRNA. ;, mRNA sequence.
ACCESSION   Al597611
VERSION     Al597611.1 GI:4506659
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 423)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL    National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
COMMENT    Unpublished (1998)
CONTACT    Contact: Robert Strausberg, Ph.D.
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from gibco.

FEATURES
source
location/Qualifiers
1..423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2167707"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn25"
notes="Organ: Brain; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTGGAGCGCGGCATAGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.: 4.71 Length: 423
Score: 99.00 Matches: 35
Percent Similarity: 44.35% Conservative: 20
Best Local Similarity: 28.23% Mismatches: 43
Query Match: 15.21% Indels: 26
DB: 9 Gaps: 7

US-09-684-215B-23 (1-128) x Al597611 (1-423)

Qy      7  PheClnLeuSerGln-----GlyGlyGlnGlyPheAlaIleProIleGlyGlnAla 23
Db      39  TTGTAAATAAGCCAAAGAGGGGCCCTGGGGCAACAGGACAGCGCGGTTCTTCAGGGG 98
Qy      24  MetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThr---ValHisIleGly 42
Db      99  TCAGGGGCATTGGGCAGATGGCTTCAGTGGGGGGGCACCCCTCCAGTCTTGTGTCA 158

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Qy      43  ProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGln 62
Db      159  CCTGGGCTGCCTCAGGGACAGGT-----GGCACTGGCTCAAAACAGGG 203
Qy      63  ArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThr 82
Db      204  TAAGCTTCGGGGGCTCACCCTCCAGCAGTTCGGA-----ACAGGCTCCTCTGGTC 257
Qy      83  AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102
Db      258  AGCATTGGGGGTTGTCGCGGTGTCGCCAGCAGTTATG----- 293
Qy      103  HisProGlyAspValIleSerValThrTrpGlnThrLysSerGly-----Gly 118
Db      294  CCCCGGGA-----TCTCTTTTGGCCACCCGTTGGGGCTGAGCCTTCTCAGG 344
Qy      119  ThrArgThrGly 122
Db      345  ACCCTTCTGGG 356

RESULT 17
Bi350520/c
LOCUS   Bi350520
DEFINITION   fr32B05.y1 zebrafish adult brain Danio rerio cDNA clone IMAGE:4955073 5' similar to SW:ACT2_FUGRU P53485 ACTIN, CYTOPLASMIC 2 ;, mRNA sequence.
ACCESSION   Bi350520
VERSION     Bi350520.1 GI:15044966
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
REFERENCE   1 (bases 1 to 499)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1. Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.edu
CDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center. Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
Seq primer: T7
High quality sequence stop: 301.
Location/Qualifiers
1..499
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4955073"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/notes="Vector: pZiPlox; Site 1: NotI; Site 2: SalI; Original library was constructed in lambdaZiPlox. Mass

```


Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: Clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 017 row: F column: 10
 Seq primer: T7 Promoter Primer.

FEATURES

Location/Qualifiers
 1..444
 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SCEZR21017F10"
 /lab_host="DH10B"
 /clone_lib="R21"

/note="Organ: Shoot-root transition zone from young plants
 (large insert library); Vector: pSport1; Site 1: SalI;
 Site 2: NotI; An unidirectional cDNA library generated
 from [Shoot-root transition zone from young plants (large
 insert library)]. cDNA was prepared from polyA+ mRNA
 using SuperScript Plasmid System Kit (Invitrogen). The
 double-strand cDNAs were fractionated in a sepharose
 CL-2B 40cm-columns and fragments sizing between 0.8 and
 1.5 Kb were directionally cloned into the vector. Details
 of each source of RNA and library construction can be
 obtained at http://sucet.lad.ic.unicamp.br/public"

ORIGIN

Alignment Scores:
 Pred. No.: 7.99 Length: 444
 Score: 97.00 Matches: 26
 Percent Similarity: 47.62% Conservative: 14
 Best Local Similarity: 30.95% Mismatches: 26
 Query Match: 14.90% Indels: 18
 DB: 13 Gaps: 2

US-09-684-215B-23 (1-128) x CA148171 (1-444)

QY 54 AsnAsnGlyAsnGlyAlaArgValGlnArgValGlySerAlaProAlaLaserLeu 73
 Db 32 AATGTTGCAACGAGCTTTATCTAAGTACCTGGGGCAGTCTCGAGCCAGGCA 91
 QY 74 GlyIleSer-----ThrGlyAspValIleThr 82
 Db 92 GGCCTTCTCGACCGCAGGGGTTTCGTGTTAACTTTCTGTGTATGTCATCGTT 151
 QY 83 AlavalAspGlyAlaProIleAsnSerAlaThraAlaMetAlaAspAlaLeuAenglyHis 102
 Db 152 GCAGTGTGATGCACAACTGTTAAGGGCAATCAGACCTGCTGAGGTTCTGGATGACTAT 211
 QY 103 HisProGlyAspValIleSerValThrTpGlnThrIysSerGlyGlyThrArgThrGly 122
 Db 212 GCGCTCGGGATCAGGTGACCTTGACA-----ATCCGGCGAGGC 250
 QY 123 AsnValThrLeu 126
 Db 251 TCTGAACCCCTC 262

RESULT 20

LOCUS B1721127 543 bp mRNA linear EST 19-SEP-2001
 DEFINITION 1031054B10.y1 C. reinhardtii CC-1690, Stress II (normalized),
 Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
 ACCESSION B1721127
 VERSION B1721127.1 GI:15696822
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii
 ORGANISM Chlamydomonas reinhardtii
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadales; Chlamydomonas.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,

Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
 Analyses of the Chlamydomonas reinhardtii Genome: A Model,
 Unicellular System for Analyzing Gene Function and Regulation in
 Vascular Plants. Project: 1031
 Unpublished (2001)
 Contact: Charles Hauser
 DCMB Box 91000
 Duke University
 Durham, NC 27708-1000
 Tel: 919 613 8159
 Fax: 919 613 8177
 Email: chauser@duke.edu.

FEATURES

Location/Qualifiers
 1..543
 /organism="Chlamydomonas reinhardtii"
 /mol_type="mRNA"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, Stress II
 (normalized), Lambda Zap II"
 /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
 XhoI; Stress condition II library, constructed by John
 Davies and Jeffrey McDermott, combines cDNAs from CC-1690
 cells grown to mid-log phase in TAP (NH4+ - containing)
 and shifted to TAP - NO3- (24hrs); H2 production
 conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
 Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
 sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
 PolyA mRNA was purified from each sample, pooled and cDNA
 synthesized. The cDNA was directionally cloned into lambda
 Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
 sites. pBluescript II SK- plasmids were excised from the
 lambda Zap clones by superinfection with ExAssist
 (Stratagene) phage. The library was normalized using
 method 4 described in Bonaldo et al., (1996) Genome
 Research 6: 791-806."

ORIGIN

Alignment Scores:
 Pred. No.: 10.7 Length: 543
 Score: 97.00 Matches: 31
 Percent Similarity: 39.83% Conservative: 16
 Best Local Similarity: 26.27% Mismatches: 49
 Query Match: 14.90% Indels: 22
 DB: 12 Gaps: 4

US-09-684-215B-23 (1-128) x B1721127 (1-543)

QY 10 SerGlnGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGln 29
 Db 153 GCATCTCCGGGTGGGCTTCGGCTGCCATCGACAGTGTGGCGGCTGTAGACCAG 212
 QY 30 IleArgSerGlyGlyGly-----SerProThrValHisIleGly-----ProThr 44
 Db 213 ATCTCTGACCTACGGCGCGGTCTGCGGCCGCTGTGGAGTGCACCTGGCGCCGCGCAG 272
 QY 45 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 64
 Db 273 GTGCTCAAGCAGCTGGG-----CAGCGGGCGGTGCTGTCTAGAGTG 317
 QY 65 ValGlySerAlaProAlaAlaSerLeuGlyIleSer-----76
 Db 318 CCCAAGGGTCCCGCGGAGAGCGCCATCAAGCCACCACCATGCGGACCGCTTCAGC 377
 QY 77 -----ThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAla 92
 Db 378 GGCTCCCTGCTGCTGGGCGCATCATCAAGCATTTGACGCGGACCGCGTAAGACTAT 437
 QY 93 ThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerVal 110
 Db 438 TCGGACCTGGTGGAGCGCTGTGATGAGAAGCGCGTGGCGGACACAGTCAAGGTG 491

RESULT 21

AW285510
LOCUS
DEFINITION
LGI_241_E05_g1_A002 Light Grown 1 (LGI) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 546)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 126
High quality sequence stop: 546
POLYA=Yes.

FEATURES
source
1..546
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LGI)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Alignment Scores:
Pred. No.: 13.5 Length: 546
Score: 96.00 Matches: 25
Percent Similarity: 47.62% Conservative: 15
Best Local Similarity: 29.76% Mismatches: 26
Query Match: 14.75% Indels: 18
DB: 10 Gaps: 2
US-09-684-215B-23 (1-128) x AW285510 (1-546)

QY 54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73
DB 56 AATGTTGGCAACGAGGCTTTATCTTAAAGGTACCTGGGGGAGCTGCGAGCCAAAGCA 115
QY 74 GlyIleSer-----ThrGlyAspValIleThr 82
DB 116 GGCTCTTGCTCCAAACCGGAGGGGTTTGTGCTGTAATATTGTTCTGGGTGATATCATCGTT 175
QY 83 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102
DB 176 GCAGTGGACGGCAACCTTTAAAGGCAAACTGACCTGCTGAGGGTTCTGGATGACTAT 235
QY 103 HisProGlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGly 122
DB 236 GCGTCGGAGATCAGGTGACCTTGACA-----ATCCGGCGAGGC 274
QY 123 AsnValThrLeu 126
DB 275 TCAGAAACCCCTT 286

RESULT 22
AW285527
LOCUS
DEFINITION
LGI_241_G05_g1_A002 Light Grown 1 (LGI) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 551)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 16
High quality sequence stop: 552
POLYA=Yes.

FEATURES
source
1..551
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LGI)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Alignment Scores:
Pred. No.: 13.7 Length: 551
Score: 96.00 Matches: 25
Percent Similarity: 47.62% Conservative: 15
Best Local Similarity: 29.76% Mismatches: 26
Query Match: 14.75% Indels: 18
DB: 10 Gaps: 2
US-09-684-215B-23 (1-128) x AW285527 (1-551)

QY 54 AsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeu 73
DB 61 AATGTTGGCAACGAGGCTTTATCTTAAAGGTACCTGGGGGAGCTGCGAGCCAAAGCA 120
QY 74 GlyIleSer-----ThrGlyAspValIleThr 82
DB 121 GGCTCTTGCTCCAAACCGGAGGGGTTTGTGCTGTAATATTGTTCTGGGTGATATCATCGTT 180
QY 83 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102
DB 181 GCAGTGGACGGCAACCTTTAAAGGCAAACTGACCTGCTGAGGGTTCTGGATGACTAT 240
QY 103 HisProGlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGly 122
DB 241 GCGTCGGAGATCAGGTGACCTTGACA-----ATCCGGCGAGGC 279
QY 123 AsnValThrLeu 126
DB 280 TCAGAAACCCCTT 291

```

US-09-684-215B-23 (1-128) x B1378928 (1-677)

QY 58 GlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThr 77
Db 143 GGAGTACTGGTGGCAGGATCATTTGGGGTGCACCTCATACAGTGGGGTATCGGTCCT 202
QY 78 GlyAspValIleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAsp 97
Db 203 GGTGACGTCATCACCAGTATCAACGGTCGATAGTGGTACGTCAGCAGACATCTACGAC 262
QY 98 AlaLeuAenGlyHisHisProGlyAspValIleSerValThr 111
Db 263 GCGGTAAATAGC-----GGCAGCAGCGTGAACATCACC 295

RESULT 24
CA975497/97
LOCUS CA975497/c
DEFINITION AGENCOURT_11067943 NCI CGAP_ZKIdl Danio rerio cDNA clone
IMAGE:6805289 5', mRNA sequence.
ACCESSION CA975497
VERSION CA975497.1 GI:27508151
KEYWORDS EST
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

CA975497 909 bp mRNA linear EST 06-JAN-2003
AGENCOURT_11067943 NCI CGAP_ZKIdl Danio rerio cDNA clone
IMAGE:6805289 5', mRNA sequence.
ACCESSION CA975497
VERSION CA975497.1 GI:27508151
KEYWORDS EST
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE
1 (bases 1 to 909)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1431 row: c column: 16
High quality sequence start: 10
High quality sequence stop: 695.

FEATURES
source
1..909
location/Qualifiers
organism="Danio rerio"
mol_type="mRNA"
db_xref="taxon:7955"
clone="IMAGE:6805289"
lab_host="DH10B (TI-resistant)"
clone_lib="NCI CGAP ZKIdl"
note="Organ: Kidney; Vector: pCMV-SPORT6.1; Site 1:
EcoRV; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo df: Average insert size 1.8 kb. Constructed by J.
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard University). Note: this is a
NCI CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 35.7 Length: 909
Score: 95.00 Matches: 38
Percent Similarity: 39.86% Conservative: 17
Best Local Similarity: 27.54% Mismatches: 55
Query Match: 14.59% Indels: 28
DB: 14 Gaps: 6

US-09-684-215B-23 (1-128) x CA975497 (1-909)
QY 9 LeuSerGlnGlyGlnGly-----PheAlaIleProIleGlyGlnAlaMetAla 25
Db 808 CTGGAAACGGGGCCCTCGGGCACTTGAACCTTCTTCACCAATGGTACCTGCTCC 749

RESULT 23
B1378928 677 bp mRNA linear EST 26-AUG-2003
LOCUS BFLG 000559 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG
or MPMPG498) Branchiostoma floridae cDNA clone MPMPG498P1235 5',
mRNA sequence.
B1378928 1 GI:30914099
B1378928 EST.
Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
1 (bases 1 to 677)
Panopoulou G., Hennig, S., Groth, D., Krause, A., Poustka, A.J.,
Herwig, R., Vigron, M. and Lehrach, H.
New evidence for genome-wide duplications at the origin of
vertebrates using an amphioxus gene set and completed animal
genomes
Genome Res. 13 (6A), 1056-1066 (2003)
22683279
PUBMED 12799346
Contact: Panopoulou G
Laboratory 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inthestr.63-73, D-14195 Berlin, Germany
Tel.: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoulou@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(CONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: http://www.molgen.mpg.de/amphioxus/
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (http://www.rzpd.de)
PCR Primers
FORWARD: 5' CCCAGCTTTACACTTTATGCTCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACCGCTGGCGGAAGGGGATGTG 3' (M13FSP)
Insert Length: 1200 Std Error: 0.00
Seq primer: 5'-CCGGTCGGATATCCCGGT-3' pSport3/86
High quality sequence stop: 677.
location/Qualifiers
1..677
organism="Branchiostoma floridae"
mol_type="mRNA"
db_xref="taxon:7739"
clone="MPMPG498P1235"
tissue_type="whole embryo"
dev_stage="5-6 hrs (gastrula stage)"
lab_host="E.coli, XL1 blue"
clone_lib="Amphioxus 5-6 hrs cDNA library (Name
convention: BFLG or MPMPG498)"
note="Vector: pSport1; Site 1: SalI, KpnI, EcoRI (5');
Site 2: NotI, BamHI, HindIII (3'); OligodT primed and
directionally cloned in pSport1 vector using a NotI
(5'-pGACATGTTCTAGATCGGAGCGGCCCC (T)15-3' and a SalI 5'-
TCGACCCAGCGTCCG-3' adapters (Gibco BRL)."
```

Qy 26 Ile-----AlaGlyGlnIleAerSerGlyGlyGlySerProThrValHisIle--- 41
 Db 748 GTCCAGGAGCTGAGTCTTCTCCAGGAGGAGGAGGAGGAGCGGTGCCATCTCTCGT 689
 Qy 42 -----GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsn 57
 Db 688 CTCAAAGTCAGGGCCACATAGCAGAGCTTCTCTGATGTCACGGACAT----- 638
 Qy 58 GlyAlaArgValGlnArgValGlySerAlaProAlaIleSerLeuGlyIleSerThr 77
 Db 637 -----TTCCCTCTCAGCTGTGGTGGTGAAGCTGTAGCTCTCTCGGTCAAGATCTT 587
 Qy 78 GlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsp 97
 Db 586 CATGAGGTAGTCAGTCAGTCACGGCAGCCAGTCAGAGGAGGATGGCGGGGCGAG 527
 Qy 98 Ala-----LeuAenGlyHisProGlyAspValIleSerValThrTrpGlnThr 114
 Db 526 GGCCTAACCTCGTAGATGGGCACAGTGTGGTGCACACCATCACAGATCCATCAGAT 467
 Qy 115 LysSerGlyGlyThrArg-----ThrGlyAsnVal 124
 Db 466 ACCAGTGTACACAGCAGGATACAGGACAGGACAGCAGCCTCGATGGCAAGTGA 413

RESULT 25
 CF787130/c
 LOCUS CF787130 600 bp mRNA linear EST 21-OCT-2003
 DEFINITION 854999 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION CF787130
 VERSION CF787130.1 GI:37791691
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 600)
 Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 Nonneman,D.J., Wray,J.E. and Keele,J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 UNPUBLISHED (2003)
 JOURNAL Contact: Smith TPL
 COMMENT USDA, ARS US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plater: TM8001 row: 1 column: 11
 Seq primer: GTAATACGATCCTATAGG.
 Location/Qualifiers
 1..600
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /issue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4PIG"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

FEATURES
 source
 1..600
 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /issue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4PIG"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 Library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN
 Alignment Scores:
 Pred. No.: 21.9 Length: 600
 Score: 94.50 Matches: 32
 Percent Similarity: 44.8% Conservative: 20
 Best Local Similarity: 27.5% Mismatches: 41
 Query Match: 14.5% Indels: 23
 DB: 14 Gaps: 6

US-09-684-215B-23 (1-128) x CF787130 (1-600)

Qy 12 GlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArg 31
 Db 554 GGGGCAACAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 495
 Qy 32 SerGlyGlyGlySerProThrVal---HisIleGlyProThrAlaPheLeuGlyLeuGly 50
 Db 494 TTGAGTGG 435
 Qy 51 ValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAla 70
 Db 434 -----GGCAGCTGGCTCAAGACGGGTAAGCTTCAGGGGGGCGCTCAGCCTCC 390
 Qy 71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsn 90
 Db 389 AGCAATCTTGGG-----ACAGCTCTCTCTGGTCAGATCGGGGGTTCATCCGTGCG 336
 Qy 91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisProGlyAspValIleSerVal 110
 Db 335 CCTGCA-----GGTATGCCCCCAGGA-----TCTCTC 309
 Qy 111 ThrTrpGlnThr-----LysSerGlyGlyThrArgThrGly 122
 Db 308 TCTGGCCAGCTGTGGGGGTGAGCATCTCTCAGGAGCCCTTCGCGT 261

RESULT 26
 BX674871/c
 LOCUS BX674871 647 bp mRNA linear EST 28-OCT-2003
 DEFINITION BX674871 Sus Scrofa library (scac) Sus scrofa cDNA clone
 scac00371.j.05 5prim, mRNA sequence.
 ACCESSION BX674871
 VERSION BX674871.1 GI:38008823
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 647)
 Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
 Soares,M., Bonaldo,F. and Hately,F.
 A Pig Normalised Multi-Tissue cDNA Library
 UNPUBLISHED (2003)
 JOURNAL Contact: Tosser-Klopp G
 COMMENT Genetique Animale
 Institut National de la Recherche Agronomique
 Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
 cedex, FRANCE
 Tel: 33 (0) 5.61.28.51.14
 Fax: 33 (0) 5.61.28.53.08
 Email: tosser@toulouse.inra.fr
 Clone distribution: AGENRE Resource centre, Francois PIUMI,
 Francois.PIUMI@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
 Genome (IREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
 FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at signasupport@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0037, row: j column: 5.
 Location/Qualifiers
 1..647
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="scac00371.j.05"
 /issue_type="mixed"
 /clone_lib="Sus Scrofa library (scac)"
 /note="Vector: pT73D-pac vector; tissues: adipose tissue,
 brain, kidney, liver, muscle, ovary, testis, heart,
 hypothalamus, pancreas, skin, spleen, thymus, placenta,
 pituitary gland, seminal vesicle, small intestine,
 uterus, adrenals, bulbo uretral gland, cerebral trunk,

FEATURES
 source
 1..647
 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="scac00371.j.05"
 /issue_type="mixed"
 /clone_lib="Sus Scrofa library (scac)"
 /note="Vector: pT73D-pac vector; tissues: adipose tissue,
 brain, kidney, liver, muscle, ovary, testis, heart,
 hypothalamus, pancreas, skin, spleen, thymus, placenta,
 pituitary gland, seminal vesicle, small intestine,
 uterus, adrenals, bulbo uretral gland, cerebral trunk,

epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Alignment Scores:
Pred. No.: 24.4 Length: 647
Score: 94.50 Matches: 32
Percent Similarity: 44.83% Conserv: 20
Best Local Similarity: 27.59% Mismatches: 41
Query Match: 14.52% Indels: 23
DB: 13 Gaps: 6

US-09-684-215B-23 (1-128) x BX674871 (1-647)

QY 12 GlyGlyGlyGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArg 31
DB 600 GGGCAACAGACAGCAGGCGCGCTCTCAGGGTCAGGGGCATTTGGCAGATCGC 541
QY 32 SerGlyGlyGlySerProThrVal---HisIleGlyProThrAlaPheLeuGlyLeuGly 50
DB 540 TTGAGTGGGGGGCGCCCTCGTGTCTCTATACCTCGGCTCGGCGACAGGT 481
QY 51 ValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAla 70
DB 480 -----GGCAGTGGCTCAAGACAGGGGTAAAGCTTCAGGGGCTCAGCCTCC 436
QY 71 AlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsn 90
DB 435 ACCAATTCGGA-----ACAGGCTCTCTGTGTCAGCATCGGGGTTCATCGGTGCG 382
QY 91 SerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisProGlyAspValIleSerVal 110
DB 381 COTGCA-----GGTATGCCCCCAGGA-----TCCTC 355
QY 111 ThrTrpGlnThr-----LysSerGlyGlyThrArgThrGly 122
DB 354 TCCTGGCCAGCTGTGGGGCTGAGCATCTTCAGGACCCCTTCGGT 307

RESULT 27
BJ285991/c 728 bp mRNA linear EST 09-APR-2002
LOCUS
DEFINITION
aestivum cDNA clone whrl3124 3', mRNA sequence.

ACCESSION
BJ285991
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)

REFERENCE
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
National Institute of Genetics
Center For Genetic Resource Information
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..728
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whrl3124"
/tissue_type="root"
/dev_stage="Peekes", scale 1"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_r"

ORIGIN

Alignment Scores:

Pred. No.: 29 Length: 728
Score: 94.50 Matches: 37
Percent Similarity: 42.22% Conserv: 20
Best Local Similarity: 27.41% Mismatches: 53
Query Match: 14.52% Indels: 25
DB: 12 Gaps: 5

US-09-684-215B-23 (1-128) x BJ285991 (1-728)

QY 10 SerGlnGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIle----- 26
DB 582 AGCTCGCGCGGTGGTGGTTTGTCTATCAATCATCACTATCAATATCAATATGTTCTCTCAG 523
QY 27 -----AlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro 43
DB 522 TTGATTCAGTCTGGAAGGTTTCGAGCTGCTGGGCTGAATGTGAATTCGACCATCCG 463
QY 44 ThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg 63
DB 462 ATTGGGTAT---CAGCTTAACTCCGTGAT-----GGTCTCTTATATCTGAAG 418
QY 64 ValValGlySerAlaProAlaAlaSerLeuGly----- 74
DB 417 GTTCCCCCGGCGAGCACCTGGAAAAGCAGGTCTAGTTCTTACAGGCGGGGTTTGGC 358
QY 75 -----IleSerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAla 92
DB 357 GGCATATTTGCTCTGGCGCACGTCATTGTTGAGTGGATGGCAACCCGATTAAAGGGCAAA 298
QY 93 ThrAlaMetAlaAspAlaLeuAsnGlyHisProGlyAspValIleSerValThrTrp 112
DB 297 TCTGACTCTGAGGTTTACAGCTACGCGGTTCGAGACACGCTGACCTGACGATC 238
QY 113 GlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeuAla 127
DB 237 AGAAGA-----GGCAGTGGACATTCGGATAGCCCTGTCG 202

RESULT 28
CC345457
LOCUS
DEFINITION
genomic survey sequence.

ACCESSION
CC345457
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5943
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..600
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0365K20"

/clone_lib="ZM_0.7.1.5_KB"
/note="vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Alignment Scores:
Pred. No.: 27.5 Length: 600
Score: 93.50 Matches: 32
Percent Similarity: 41.58% Conservative: 10
Best Local Similarity: 31.68% Mismatches: 48
Query Match: 14.36% Indels: 11
DB: 28 Gaps: 2

US-09-684-215B-23 (1-128) x CC345457 (1-600)

QY 13 GlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer 32
DB 303 GGCATTGTTTTTGGCAATCCGCGCTGGCGACCAAAATATGATAGCTGATTCGC 362
QY 33 GlyGlyGlySerProThrValHisIleGlyProThrAlaPheLeuGlyValVal 52
DB 363 GATGCCGGGTGATCCGGGTATATCGGTATTACC-----GGCGGAGCTCGC 413
QY 53 AspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGly-----66
DB 414 CGGTGACCGCTCAGCGGCGAGCAACCTCGATCGGTGCGAGGCATTATTGTAGTAAAGTG 473
QY 67 -----SerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 84
DB 474 ACGCGCGCGGTCCGGCGGATCGCGCGGCATCAGGCCAATGATGCTCTCGCTCGAGGTA 533
QY 85 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 104
DB 534 AACGGTAAGCGCGGCTGTCGCGCGGAGAGACCATGGACAGGTGGCGGAATCCGCCCG 593
QY 105 Gly 105
DB 594 GGA 596

RESULT 29
LOCUS CA471201/c 907 bp mRNA linear EST 12-NOV-2002
DEFINITION AGENCOURT_10698245 NCI_CGAP_ZkId1 Danio rerio cDNA clone
IMAGE:6791062 5', mRNA sequence.

CA471201

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 907)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14294 row: b column: 21

High quality sequence stop: 590.

Location/Qualifiers

1. 907

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:6791062"

FEATURES
source

/lab_host="DH10B (T1-resistant)"
/clone_lib="NCI_CGAP_ZkId1"
/note="Organ: kidney; Vector: pCMV-SPORT6.1; Site 1:
EcoRV; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.8 kb. Constructed by J.
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard University). Note: this is a
NCI_CGAP Library."

ORIGIN

Alignment Scores:
Pred. No.: 50.1 Length: 907
Score: 93.50 Matches: 32
Percent Similarity: 41.18% Conservative: 17
Best Local Similarity: 26.88% Mismatches: 53
Query Match: 14.36% Indels: 17
DB: 14 Gaps: 4

US-09-684-215B-23 (1-128) x CA471201 (1-907)

QY 12 GlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIle-----AlaGly 28
DB 847 GGCACCTTGAACCTTTCATTTGCCCAATGGTGTATGATGCCCTGTCGTCAGGAGCTGTAGCT 788
QY 29 GlnIleArgSerGlyGlyGlySerProThrValHisIle-----GlyPro 43
DB 787 CTTTCTCCAGGAGGAGGAGGAGGAGCGGTGCCCATCTCTCTTCAAAGTCAAGGCGCAC 728
QY 44 ThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArg 63
DB 727 ATAGCAGACCTTCTCTCTGATGTCACGGACAA-----TTCCCTCTC 686
QY 64 ValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAla 83
DB 685 AGCTGTGGTGGTGAAGCTGTAGCTCTCTCGTCAGGATCTTCATCAGGTAGTCAGTCAG 626
QY 84 ValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAla-----LeuAsn 100
DB 625 GTCACGCCCGCAGCAAGTCCAGACGAGGATGGCATGGCGCGCGGTAAACCTCTGTAGAT 566
QY 101 GlyHisHisProGlyAspValIleSerValThrTptGlnThrLysSerGlyGlyThr 119
DB 565 GGGCACAGTGTGGTGACCATCACCATCAGGAGTCCATCAGATACCAGGTGTAGGACC 509

RESULT 30
LOCUS CF265501/c

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 913)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Len Zon, Harvard

cDNA Library Preparation: Open Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L14M14682 row: j column: 09
High quality sequence stop: 620.
Location/Qualifiers
1. .913
source

FEATURES

/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6996778"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_7"
/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH_ZGC_10). Library was constructed by
Open Biosystems (Huntsville, AL)"

ORIGIN

Alignment Scores:					
Pred. No.:	50.6	Length:	913		
Score:	93.50	Matches:	37		
Percent Similarity:	37.96%	Conservative:	15		
Best Local Similarity:	27.01%	Mismatches:	56		
Query Match:	14.36%	Indels:	29		
DB:	14	Gaps:	5		

US-09-684-215B-23 (1-128) x CF265501 (1-913)

Qy	11	GlnGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIle	30
Db	826		
Qy	31	Arg	41
Db	786		
Qy	42	-----GlyProThrAlaPheLeuGlyValValAlaAspAsnAsnGlyAsnGly	58
Db	706		
Qy	59	AlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGly	78
Db	658		
Qy	79	AspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAla	98
Db	604		
Qy	99	-----LeuAsnGlyHisProGlyAspValIleSerValThrTrpGlnThrLys	115
Db	544		
Qy	116	SerGlyGlyThrArg	124
Db	484		

Search completed: April 30, 2004, 04:41:02
Job time : 2510.02 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 22:28:57 ; Search time 65.5311 Seconds
(without alignments)
1083.969 Million cell updates/sec

Title: US-09-684-215B-23

Perfect score: 651
Sequence: 1 TAADNQLSQGGGFAIPI.....SVTWQTKSGGTRGNVTLAE 128

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO_spool/US09684215/runat_29042004_061306_13249/app_query.fasta_1.1180
-DB=issued Patents NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09684215@cgn 1 1.115 @runat_29042004_061306_13249 -NCPUS=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	100.0	702	4	US-09-287-849-27
2	651	100.0	2287	4	US-09-223-040-1
3	651	100.0	2287	4	US-09-287-849-1
4	651	100.0	4403765	3	US-09-103-840A-2
5	651	100.0	4411529	3	US-09-103-840A-1
6	646	99.2	447	3	US-08-818-112-4
7	646	99.2	447	4	US-08-818-111-4
8	646	99.2	447	4	US-09-056-556-4
9	646	99.2	447	4	US-09-072-598-4
10	646	99.2	447	4	US-09-072-967-4
11	646	99.2	1872	3	US-08-818-112-17
12	646	99.2	1872	4	US-08-818-111-17

ALIGNMENTS

RESULT 1

US-09-287-849-27

Sequence 27, Application US/09287849
Patent No. 6621198
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-0090200S
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 27
LENGTH: 702
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
OTHER INFORMATION: protein Rail2-DPPD (Designated Mtb24), reading
OTHER INFORMATION: frame 1

Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 822, App
Sequence 822, App
Sequence 822, App
Sequence 1862, App
Sequence 353, App
Sequence 353, App
Sequence 353, App
Sequence 834, App
Sequence 834, App
Sequence 1861, App
Sequence 351, App
Sequence 351, App
Sequence 851, App
Sequence 851, App
Sequence 348, App
Sequence 348, App
Sequence 332, App
Sequence 332, App
Sequence 188, App
Sequence 188, App
Sequence 188, App
Sequence 352, App
Sequence 352, App
Sequence 336, App
Sequence 336, App
Sequence 308, App
Sequence 308, App
Sequence 324, App
Sequence 324, App
Sequence 316, App
Sequence 316, App
Sequence 340, App

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; NAME/KEY: CDS
; LOCATION: (1)...(693)
; OTHER INFORMATION: bi-fusion protein Ra12-DPPD (designated Mlb24),
; OTHER INFORMATION: reading frame 1
; NAME/KEY: CDS
; LOCATION: (2)...(700)
; OTHER INFORMATION: reading frame 2
; NAME/KEY: CDS
; LOCATION: (3)...(701)
; OTHER INFORMATION: reading frame 3
US-09-287-849-27

Alignment Scores:
Pred. No.: 4,036-64 Length: 702
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-287-849-27 (1-702)
QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGCTGGGCGAGGATTCCGCATTCCGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 85 GGCAGGCGATGCGGATCCGCGGCGAGATCCGATCGGGTGGGGGTCCACCACCGTTTCAT 144
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 145 ATCGGCGCTACCGCTTCTCCGCTGGGTGTTGTCGACAAACACGCGGCGACGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 205 GTCCACGCGTGGTTCGGGAGCGCTCCGGCGGCAAGTCTCCGATCTCCACCGCGGACGTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 265 ATCACCGCGTGCACGCGCTCCGATCACTCGGCCACCGCATGGCGGACGCGCTTAAC 324
QY 101 GlyHisHieProGlyAspValIleSerValThrTrpGlnThrIlySerGlyThrArg 120
Db 325 GGGCATCATCCCGTGACGTCTCCGTGACCTGGTGCACCAACCAAGTCCGGCGGCGCGGT 384
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 385 ACAGGGAACGTGACATTGGCCGAG 408

RESULT 2
US-09-223-040-1
; Sequence 1, Application US/09223040
; Patent No. 6544522
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE REFERENCE: 014058-009010US
; CURRENT APPLICATION NUMBER: US/09/223,040
; CURRENT FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
; OTHER INFORMATION: protein Ra12-TbH9-Ra35

; NAME/KEY: modified_base
; LOCATION: (30)
; OTHER INFORMATION: n = g, a, c or t
; NAME/KEY: modified_base
; LOCATION: (33)
; OTHER INFORMATION: n = g, a, c or t
; NAME/KEY: CDS
; LOCATION: (42)...(2231)
; NAME/KEY: modified_base
; LOCATION: (2270)
; OTHER INFORMATION: n = g, a, c or t
US-09-223-040-1

Alignment Scores:
Pred. No.: 1,92e-63 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-223-040-1 (1-2287)
QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 63 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGCTGGGCGAGGATTCCGCATTCCGATC 122
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 123 GGCAGGCGATGCGGATCCGCGGCGAGATCCGATCGGGTGGGGGTCCACCACCGTTTCAT 182
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 183 ATCGGCGCTACCGCTTCTCCGCTGGGTGTTGTCGACAAACACGCGGCGACGA 242
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCACGCGTGGTTCGGGAGCGCTCCGGCGGCAAGTCTCCGATCTCCACCGCGGACGTG 302
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 303 ATCACCGCGTGCACGCGCTCCGATCACTCGGCCACCGCATGGCGGACGCGCTTAAC 362
QY 101 GlyHisHieProGlyAspValIleSerValThrTrpGlnThrIlySerGlyThrArg 120
Db 363 GGGCATCATCCCGTGACGTCTCCGTGACCTGGTGCACCAACCAAGTCCGGCGGCGCGGT 422
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTGGCCGAG 446

RESULT 3
US-09-287-849-1
; Sequence 1, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Devin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
```

APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (42)..(2231)
NAME/KEY: modified_base
LOCATION: (2270)
OTHER INFORMATION: n = g, a, c or t
US-09-287-849-1

Alignment Scores:
Pred. No.: 1.92e-63 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-287-849-1 (1-2287)

Qy 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 63 ACGGCGCGTCCGATACTTCAGCTGCCAGGGTGGCAGGAGTTCGCCATCCGATC 122
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 123 GGGCAGGCGATGGCGATCGCGGCGCAGATCGATCGGGTGGGGGTTCACCCACCGTTTCAT 182
Qy 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyValAlaArg 60
Db 183 ATCGGGCGCTACCGCTTCCTCGGCTTGGGTGTTCGACAAACACGCGCACGCA 242
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCACCGCGTGGTGGAGCGCTCCGCGCGCAAGTCTCGCATCTCCACCGCGCGAGTG 302
Qy 81 IleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 303 ATCACCGCGTCCGCGCTCCGATCAACTCGGCGCACCGCGATGGCGGACGCGCTTAAC 362
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 363 GGGCATCATCCGGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCGGCGGACCGGT 422
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTGGCCGAG 446

RESULT 4
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 4.17e-59 Length: 4403765
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-103-840A-2 (1-4403765)

Qy 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 151984 ACGGCGCGTCCGATACTTCAGCTGCCAGGGTGGCAGGAGTTCGCCATCCGATC 152043
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 152044 GGGCAGGCGATGGCGATCGCGGCGCAGATCGATCGGGTGGGGGTTCACCCACCGTTTCAT 152103
Qy 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyValAlaArg 60
Db 152104 ATCGGGCGCTACCGCTTCCTCGGCTTGGGTGTTCGACAAACACGCGCACGCA 152163
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 152164 GTCCACCGCGTGGTGGAGCGCTCCGCGCGCAAGTCTCGCATCTCCACCGCGCGAGTG 152223
Qy 81 IleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 152224 ATCACCGCGTCCGCGCGCTCCGATCAACTCGGCGCACCGCATGGCGGACGCGCTTAAC 152283
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 152284 GGGCATCATCCGGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCGGCGGCGCACGCGT 152343
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 152344 ACAGGGAACGTGACATTGGCCGAG 152367

RESULT 5
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

PRIOR APPLICATION NUMBER: US 09/056,556
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2287
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (42)..(2231)
NAME/KEY: modified_base
LOCATION: (2270)
OTHER INFORMATION: n = g, a, c or t
US-09-287-849-1

Alignment Scores:
Pred. No.: 1.92e-63 Length: 2287
Score: 651.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-287-849-1 (1-2287)

Qy 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 63 ACGGCGCGTCCGATACTTCAGCTGCCAGGGTGGCAGGAGTTCGCCATCCGATC 122
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 123 GGGCAGGCGATGGCGATCGCGGCGCAGATCGATCGGGTGGGGGTTCACCCACCGTTTCAT 182
Qy 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyValAlaArg 60
Db 183 ATCGGGCGCTACCGCTTCCTCGGCTTGGGTGTTCGACAAACACGCGCACGCA 242
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 243 GTCCACCGCGTGGTGGAGCGCTCCGCGCGCAAGTCTCGCATCTCCACCGCGCGAGTG 302
Qy 81 IleThrAlaValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 303 ATCACCGCGTCCGCGCTCCGATCAACTCGGCGCACCGCGATGGCGGACGCGCTTAAC 362
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 363 GGGCATCATCCGGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCGGCGGACCGGT 422
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 423 ACAGGGAACGTGACATTGGCCGAG 446

RESULT 4
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND

STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-4

Alignment Scores:
Pred. No.: 8,06e-64 Length: 447
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-08-818-111-4 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGCGTCCGATTAACCTCCAGCTGCCAGGGTGGCAGGGATTCGCCATTCGGATC 70

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 131 ATCGGGCTACCGCTTCCCTCGGCTGGGTGTGTCGACAAACACGCGCACGCA 190

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 131 GTCCACCGCGTGGTGGGAGCGCTCCGCGCAGATCTCCGATCTCCACCGCGACGTG 250

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCACCAGCGGTGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 310

Qy 101 GlyHisHisProGlyAspValIleSerValThrTTPGlnThrLysSerGlyGlyThrArg 120
Db 311 GGGCATATCCCGTGAGTGTATCTCGTGAACTGGCAACCAAGTCGGGCGGCACGCGT 370

RESULT 8
US-09-056-556-4
Sequence 4, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.

US-09-684-215B-23 (1-128) x US-09-056-556-4 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGCGTCCGATTAACCTCCAGCTGCCAGGGTGGCAGGGATTCGCCATTCGGATC 70

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGCGATGCGCATCGCGGCCAGATCCGATCGGGTGGGGGTACCCACCGTTTAT 130

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValAlaAspAsnGlyAsnGlyAlaArg 60
Db 131 ATCGGCGCTACCGCTTCCCTCGGCTGGGTGTGTCGACAAACACGCGCACGCA 190

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACCGCGTGGTGGGAGCGCTCCGCGCAGATCTCCGATCTCCACCGCGACGTG 250

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCACCAGCGGTGACGCGCTCCGATCAACTGGCCACCGCGATGGCGGACGCGCTTAAC 310

Qy 101 GlyHisHisProGlyAspValIleSerValThrTTPGlnThrLysSerGlyGlyThrArg 120
Db 311 GGGCATATCCCGTGAGTGTATCTCGTGAACTGGCAACCAAGTCGGGCGGCACGCGT 370

RESULT 9
US-09-072-596-4

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; Sequence 4, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-072-596-4
Alignment Scores:
Pred. No.: 8,06e-64 Length: 447
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

US-09-684-215b-23 (1-128) x US-09-072-596-4 (1-447)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGCGTCCGATTAACCTCCAGCTGTCGCGGAGGAGTCCGCAATTCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGCGAGCGATGCGATCGCGGSCCAGATCCGATCGGTGGGGTCCACCCACCGTTCAT 130
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 131 ATCGGGCGCTACCGCTTCCTCGGCTTGGGTGTGTGTCGACAAACAGCGACGCGCAGCA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACCGTGTGCGGAGCGTTCGGCGGCGAGTCTCGGCATCTCCACCGCGGCGG 250
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

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Db 251 ATCACCAGGTCGACGGCGCTCCGATCAACTCGGCCACCGGATCGCGGACGCGTTAAC 310
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 311 GGGCATCATCCGCGTGAAGTCTATCTCGGTGAATCGGCAACCAAGTCGGCGGCGCGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 371 ACAGGAACGTCGACATTGGCCGAG 394

RESULT 10
US-09-072-967-4
; Sequence 4, Application US/09072967
; Patent No. 6592877
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-072-967-4
Alignment Scores:
Pred. No.: 8,06e-64 Length: 447
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

US-09-684-215b-23 (1-128) x US-09-072-967-4 (1-447)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGCGTCCGATTAACCTCCAGCTGTCGCGGAGGAGTCCGCAATTCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40

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Db 71 GGGCAGCGGATGGCGATCGGGGCGAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCAAT 130
Qy 41 ILeGlyPtoThrAlaPheLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 131 ATCCGGGCTACCGCTTCTCCGGCTTGGGTGTTCGACAAACAGCGACGGCGACGA 190
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 250
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCACCGCGGTGCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGGCTTAAC 310
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlyssSerGlyGlyThrArg 120
Db 311 GGGCATCATCCGGTGAGTCACTCGTGAACTGGCAACCAAGTCGGGGCGGACCGGT 370
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 371 ACAGGGAACGTGACATTGGCCGAG 394

RESULT 11
US-08-818-112-17
; Sequence 17, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-112-17
Alignment Scores:
Pred. No.: 5.34e-63 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0

Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 3 Gaps: 0
US-09-684-215B-23 (1-128) x US-08-818-112-17 (1-1872)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 758 ACGGCGCGGTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCCGCATTCGGATC 817
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGCGGATCGGATCGCGGCGCAATCCGATCGGTGGGGGTCAACCCACCGTTTCAAT 877
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 878 ATCGGGCTTACCGCTTCTCCGGCTTGGGTGTTCGACAAACAGCGCAACGGCGCACGA 937
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 938 GTCCAAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 997
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCACCGCGGTGCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGGCTTAAC 1057
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlyssSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGGTGACATCATCTCGGTGAACTGGCAACCAAGTCGGGGCGGACCGGT 1117
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 1118 ACAGGGAACGTGACATTGGCCGAG 1141
RESULT 12
US-08-818-111-17
; Sequence 17, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,111
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-17
Alignment Scores:
Pred. No.: 5.34e-63 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservativeness: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-23 (1-128) x US-08-818-111-17 (1-1872)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACAGCGCGGTCCGATAACTTCCAGCTGTCAGAGGTGGCGAGGATTCGCCATTCCGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGCGGTCCGATCGCGGCGCAATCCGATCGGTGGGGGTCCGCCATTCAT 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyValaArg 60
Db 878 ATCGGCGCTACCGCTTCTCGCTTGGGTGTGTGCGACACACGCGACGCGCAGCA 937
QY 61 ValGlnArgValValGlySerAlaProAlaIleSerGlyGlyGlyGlySerGlyGlyVal 80
Db 938 GTCCACCGGTTCGAGCGCTCCGATCACTCGGCGCAAGTCTCGCATCTCCACCGCGCGT 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCAGCGCGGTTCGAGCGCTCCGATCACTCGGCGCAAGTCTCGCATCTCCACCGCGCGT 1057
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGGTGAGTCATCTCGGTGAAGTGGCAACCAAGTCCGGCGGCGACGCGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 1118 ACAGGGAAGTGCATTTGGCCGAG 1141
RESULT 13
US-09-056-556-17
Sequence 17, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-17
Alignment Scores:
Pred. No.: 5.34e-63 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservativeness: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-23 (1-128) x US-09-056-556-17 (1-1872)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACAGCGCGGTCCGATAACTTCCAGCTGTCAGAGGTGGCGAGGATTCGCCATTCCGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGCGGTCCGATCGCGGCGCAATCCGATCGGTGGGGGTCCGCCATTCAT 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyValaArg 60
Db 878 ATCGGCGCTACCGCTTCTCGCTTGGGTGTGTGCGACACACGCGACGCGCAGCA 937
QY 61 ValGlnArgValValGlySerAlaProAlaIleSerGlyGlyGlyGlySerGlyGlyVal 80
Db 938 GTCCACCGGTTCGAGCGCTCCGATCACTCGGCGCAAGTCTCGCATCTCCACCGCGCGT 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCAGCGCGGTTCGAGCGCTCCGATCACTCGGCGCAAGTCCGATCGCGCGCGCTTAAC 1057
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGGTGAGTCATCTCGGTGAAGTGGCAACCAAGTCCGGCGGCGACGCGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 1118 ACAGGGAAGTGCATTTGGCCGAG 1141
RESULT 14
US-09-072-596-17
Sequence 17, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
TUBERCULOSIS

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1872 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-072-596-17

Alignment Scores:
Pred. No.: 5,34e-63 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-072-596-17 (1-1872)
QY 1 ThrAlaIaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACGGCGCGTCCGATTAATTCACGCTGTCAGGCTGCGGAGGATTCGCCATTCGGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGCGGATGGGATCGCGGCAATTCGATCGGCTGGGGGTGACCCACCGTTTCAT 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArg 60
Db 878 ATCCGCGCTACCGCTTCCTCGGCTTGGGTGTTGTCGACAAACACGCGCAACGGCGCAG 937
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 938 GTCCAAACGGTGGTGGAGCGCTCCGCGCAAGTCTCGGCATCTCCACCGCGCGCTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCCGCGCTACCGCTTCCTCGGCTTGGGTGTTGTCGACAAACACGCGCAACGGCGCAG 1057
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGGTGACGTCTCTCGGTGAATGGCAACCAAGTGGCGCGGCGCGCT 1117
QY 121 ThrGlyAsnValThrIleuAlaGlu 128
Db 1118 ACAGGGAACGTGACATTGGCGGAG 1141

RESULT 15
US-09-072-967-17
; Sequence 17, Application US/09072967
; Patent No. 6592877
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.

```

```

; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1872 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-072-967-17

Alignment Scores:
Pred. No.: 5,34e-63 Length: 1872
Score: 646.00 Matches: 127
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-23 (1-128) x US-09-072-967-17 (1-1872)
QY 1 ThrAlaIaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACGGCGCGTCCGATTAATTCACGCTGTCAGGCTGCGGAGGATTCGCCATTCGGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGCGGATGGGATCGCGGCAATTCGATCGGCTGGGGGTGACCCACCGTTTCAT 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArg 60
Db 878 ATCCGCGCTACCGCTTCCTCGGCTTGGGTGTTGTCGACAAACACGCGCAACGGCGCAG 937
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 938 GTCCAAACGGTGGTGGAGCGCTCCGCGCAAGTCTCGGCATCTCCACCGCGCGCTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCCGCGCTACCGCTTCCTCGGCTTGGGTGTTGTCGACAAACACGCGCAACGGCGCAG 1057
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGGTGACGTCTCTCGGTGAATGGCAACCAAGTGGCGCGGCGCGCT 1117
QY 121 ThrGlyAsnValThrIleuAlaGlu 128
Db 1118 ACAGGGAACGTGACATTGGCGGAG 1141

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Db 1118 ACAGGGAACGTGACATTGGCCGAG 1141

RESULT 16

US-09-636-215-822
; Sequence 822, Application US/09636215
; Patent No. 6620522
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 822

; LENGTH: 675

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-636-215-822

Alignment Scores: 2,48e-59 Length: 675
Pred. No.: 608.00 Matches: 122
Score: 608.00
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.39% Indels: 4
DB: Gaps: 1

US-09-684-215B-23 (1-128) x US-09-636-215-822 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCTCCGATTAACCTCCAGCTGCCAGGGTGGCAGGGATTGCCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 82 GGGCAGCGCATGCGCATCGGGGCCAGATCAAG-----CTTCCACCGCTTCAT 129
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyAsnGlyValAlaArg 60
Db 130 ATCGGGCCCTACCGCTCTCTCGGCTGGGTGTGTCGACAAACACGGCAGCGCAGCA 189
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 190 GTCCAAACGGGTGTGCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGCAGCTG 249
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACCAGCGGTTCAGCGCGCTCCGATCAACTCGGCCACCGCATGGCGGCGCTTAA 309
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyGlyThrArg 120
Db 310 GGGCATCATCCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGCGGCGCAGCGT 369
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 370 ACAGGGAACGTGACATTGGCCGAG 393

RESULT 17

US-09-685-166A-822
; Sequence 822, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21

; CURRENT APPLICATION NUMBER: US/09/685,166A

; CURRENT FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 898

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 822

; LENGTH: 675

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-685-166A-822

Alignment Scores: 2,48e-59 Length: 675
Pred. No.: 608.00 Matches: 122
Score: 608.00
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.39% Indels: 4
DB: Gaps: 1

US-09-684-215B-23 (1-128) x US-09-685-166A-822 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCTCCGATTAACCTCCAGCTGCCAGGGTGGCAGGGATTGCCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 82 GGGCAGCGCATGCGCATCGGGGCCAGATCAAG-----CTTCCACCGCTTCAT 129
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyAsnGlyValAlaArg 60
Db 130 ATCGGGCCCTACCGCTCTCTCGGCTGGGTGTGTCGACAAACACGGCAGCGCAGCA 189
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 190 GTCCAAACGGGTGTGCGGAGCGCTCCGGCGCAAGTCTCGCATCTCCACCGCGCAGCTG 249
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACCAGCGGTTCAGCGCGCTCCGATCAACTCGGCCACCGCATGGCGGCGCTTAA 309
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyGlyThrArg 120
Db 310 GGGCATCATCCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGCGGCGCAGCGT 369
Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 370 ACAGGGAACGTGACATTCGGCCGAG 393

RESULT 18

US-09-736-457-1862

Sequence 1862 Application US/09736457

Patent No. 6509448

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Kalos, Michael A.

APPLICANT: Fanger, Gary

APPLICANT: Vedvick, Tom

APPLICANT: Carter, Darick

APPLICANT: Retter, Marc

APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

APPLICANT: Wang, Aijun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.478C15

CURRENT APPLICATION NUMBER: US/09/736,457

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 1864

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1862

LENGTH: 822

TYPE: DNA

ORGANISM: Homo sapiens

US-09-736-457-1862

Alignment Scores:

Pred. No.: 3,22e-59 Length: 822

Score: 608.00 Matches: 122

Percent Similarity: 96.09% Conservativeness: 1

Best Local Similarity: 95.31% Mismatches: 1

Query Match: 93.39% Indels: 4

DB: Gaps: 1

US-09-684-215B-23 (1-128) x US-09-736-457-1862 (1-822)

Qy 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20

Db 22 ACAGCGCGTCCGATACCTCCAGGCTGTCACAGGCTGGGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40

Db 82 GGGCAGCGATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGTTTCAT 129

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAsnGlnGlyValAlaArg 60

Db 130 ATCCGGCGCTACCGCTTCCTCCGCTGGGTGTTCGACAAACACGCGACGCGACGA 189

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 190 GTCCACGCGTGGTGGGAGCGCTCCGCGCGCAAGTCTCGGCATCTCCACCGCGACGTG 249

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

Db 250 ATCACCGCGTGGCGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309

Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

Db 310 GGGCATCATCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGCGCGCACGCGT 369

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 370 ACAGGGAACGTGACATTCGGCCGAG 393

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 353

LENGTH: 900

TYPE: DNA

ORGANISM: Homo sapiens

US-09-643-597-353

Alignment Scores:

Pred. No.: 3,63e-59 Length: 900

Score: 608.00 Matches: 122

Percent Similarity: 96.09% Conservativeness: 1

Best Local Similarity: 95.31% Mismatches: 1

Query Match: 93.39% Indels: 4

DB: Gaps: 1

US-09-684-215B-23 (1-128) x US-09-643-597-353 (1-900)

Qy 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20

Db 22 ACAGCGCGTCCGATACCTCCAGGCTGTCACAGGCTGGGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40

Db 82 GGGCAGCGATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGTTTCAT 129

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAlaAsnGlnGlyValAlaArg 60

Db 130 ATCCGGCGCTACCGCTTCCTCCGCTGGGTGTTCGACAAACACGCGACGCGACGA 189

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 190 GTCCACGCGTGGTGGGAGCGCTCCGCGCGCAAGTCTCGGCATCTCCACCGCGACGTG 249

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

Db 250 ATCACCGCGTGGCGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 309

Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

Db 310 GGGCATCATCCGGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGCGCGCACGCGT 369

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 370 ACAGGGAACGTGACATTCGGCCGAG 393

RESULT 20

US-09-606-421B-353

Sequence 353, Application US/09606421B

Patent No. 6511315

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 353
LENGTH: 900
TYPE: DNA
ORGANISM: Homo sapiens
US-09-606-421B-353

Alignment Scores:
Pred. No.: 3,636-59 Length: 900
Score: 608.00 Matches: 122
Percent Similarity: 96.09%
Best Local Similarity: 95.31%
Query Match: 93.39%
DB: 4

US-09-684-215B-23 (1-128) x US-09-606-421B-353 (1-900)

QY 1 ThrAlaAlaSerAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCCGGTCGGAATACTTCCAGCTGTCCAGGTCGGCAGGATTCGCCATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGCGGATGGGATCGCGGGCCAGATCAAG-----CTTCCACCGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAsnGlyValAlaArg 60
Db 130 ATCCGGCTACCGCTTCTCCGCTTGGGTGTTCGACAAACACGGCAGCGGCACGA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 190 GTCCACCGCTGTCGGGAGGCTCCGCGGCAAGTCTCGCATCTCCACCGCGCGTG 249
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACCAGCGTCGACGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGCGCTAAC 309
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 310 GGGCATCATCCCGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCACGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 370 ACAGGGAACGTGACATTGGCCGAG 393

RESULT 21
US-09-636-215-834
Sequence 834, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hopley, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 834
LENGTH: 915
TYPE: DNA
ORGANISM: Homo sapiens
US-09-636-215-834

Alignment Scores:
Pred. No.: 3,716-59 Length: 915
Score: 608.00 Matches: 122
Percent Similarity: 96.09%
Best Local Similarity: 95.31%
Query Match: 93.39%
DB: 4

US-09-684-215B-23 (1-128) x US-09-636-215-834 (1-915)

QY 1 ThrAlaAlaSerAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCCGGTCGGAATACTTCCAGCTGTCCAGGTCGGCAGGATTCGCCATCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGCGGATGGGATCGCGGGCCAGATCAAG-----CTTCCACCGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAsnGlyValAlaArg 60
Db 130 ATCCGGCTACCGCTTCTCCGCTTGGGTGTTCGACAAACACGGCAGCGGCACGA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 190 GTCCACCGCTGTCGGGAGGCTCCGCGGCAAGTCTCGCATCTCCACCGCGCGTG 249
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACCAGCGTCGACGCGCTCCGATCAACTCGGCCACCGGATGGCGGACGCGCTAAC 309
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 310 GGGCATCATCCCGTGAGCTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCACGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 370 ACAGGGAACGTGACATTGGCCGAG 393

RESULT 22
US-09-685-166A-834
Sequence 834, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel

```
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 834
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-834

Alignment Scores:
Pred. No.: 3,71e-59 Length: 915
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.39% Indels: 4
DB: 4 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-685-166A-834 (1-915)
QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAAATCCAGCTGTCACAGGTCGGCAGGATTCGCCATTCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 82 GGGCAGCGATGCGATCGCGGCCAGATCAAG-----CTTCCCACCGTTTCA 129
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 130 ATCGGCGCTACCGCTTCTCCGCTTGGTGTGTCGACAAACGCAACGGCGCACGA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 190 GTCCAAACGGGTGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGCGAGTG 249
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 250 ATCACCAGCGTTCGACGGGCTCCGATCACTCGCCACCGGATGGCGGCGCTTAAC 309
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyGlyThrArg 120
Db 310 GGGCATCATCCCGTGACGTCATCTCGTGACCTGGCAAAACCAAGTCGGGCGGACGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
Db 370 ACAGGGAACGTGACATTGGCCGAG 393

RESULT 23
US-09-736-457-1861
; Sequence 1861, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Derrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 351
; LENGTH: 1012
; TYPE: DNA
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ORGANISM: Homo sapiens
US-09-643-597-351

Alignment Scores:
Pred. No.: 4,24e-59
Score: 608.00
Percent Similarity: 96.09%
Conservative: 1
Best Local Similarity: 95.31%
Query Match: 93.39%
DB: 4
Indels: 4
Gaps: 1

US-09-684-215B-23 (1-128) x US-09-606-421B-351 (1-1012)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 67 ACGGCCGCTCCGATTAATTCAGCTCTCCAGGGTGGCAGGATTCGCCATTCGATC 126
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 127 GGGCAGCGCATGGCGATCGGGCCAGATCAAG-----CTTCCACCGCTTCAT 174
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValValAspAsnGlyAlaArg 60
DB 175 ATCGGGCTACCGCTTCCTCGGCTTGGGTGTGTGACAAACCGGACGGCGCAGCA 234
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 235 GTCCAAACGCTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGCGAGTG 294
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 295 ATCACCAGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGCGAGTG 354
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlySerGlyValThrArg 120
DB 355 GGGCATCATCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACCGGT 414
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 415 ACAGGGAACGTGACATTGGCCGAG 438

RESULT 26
US-09-638-215-851
; Sequence 851, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-851

Alignment Scores:
Pred. No.: 5,32e-59
Score: 608.00
Percent Similarity: 96.09%
Conservative: 1
Best Local Similarity: 95.31%
Length: 1203
Matches: 122
Mismatch: 1

ORGANISM: Homo sapiens
US-09-643-597-351

Alignment Scores:
Pred. No.: 4,24e-59
Score: 608.00
Percent Similarity: 96.09%
Conservative: 1
Best Local Similarity: 95.31%
Query Match: 93.39%
DB: 4
Indels: 4
Gaps: 1

US-09-684-215B-23 (1-128) x US-09-643-597-351 (1-1012)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 67 ACGGCCGCTCCGATTAATTCAGCTCTCCAGGGTGGCAGGATTCGCCATTCGATC 126
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 127 GGGCAGCGCATGGCGATCGGGCCAGATCAAG-----CTTCCACCGCTTCAT 174
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValValAspAsnGlyAlaArg 60
DB 175 ATCGGGCTACCGCTTCCTCGGCTTGGGTGTGTGACAAACCGGACGGCGCAGCA 234
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 235 GTCCAAACGCTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGCGAGTG 294
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 295 ATCACCAGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACGGGCGAGTG 354
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlySerGlyValThrArg 120
DB 355 GGGCATCATCCGGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGGCGGACCGGT 414
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 415 ACAGGGAACGTGACATTGGCCGAG 438

RESULT 25
US-09-606-421B-351
; Sequence 351, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 351
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-351

Alignment Scores:
Pred. No.: 4,24e-59
Score: 608.00
Percent Similarity: 96.09%
Conservative: 1
Best Local Similarity: 95.31%
Length: 1012
Matches: 122
Mismatch: 1


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Query Match: 93.39% Indels: 4
DB: 4 Gaps: 1
US-09-684-215B-23 (1-128) x US-09-685-166A-851 (1-1203)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATTAATTCAGCTGTCACAGGTGGCAGGATTCGCCATTCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
DB 82 GGGCAGCGCATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAlaArg 60
DB 130 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACACACACGCGGCGCAGCA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 190 GTCCAAACGGTGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 249
QY 81 IleThrAlaValAspGlyValProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 250 ATCACCAGCGTGCAGCGCTCCGATCACTCGGCCACCGGATGGCGGCGCTTAAC 309
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 310 GGGCATCATCCCGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 370 ACAGGAGCGTGACATGGCCGAG 393

RESULT 27
US-09-685-166A-851
; Sequence 851, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-851

Alignment Scores:
Pred. No.: 5,32e-59 Length: 1203
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.31% Indels: 1
DB: 4 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-685-166A-851 (1-1203)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATTAATTCAGCTGTCACAGGTGGCAGGATTCGCCATTCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
DB 82 GGGCAGCGCATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAlaArg 60
DB 130 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACACACACGCGGCGCAGCA 189
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 190 GTCCAAACGGTGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 249
QY 81 IleThrAlaValAspGlyValProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 250 ATCACCAGCGTGCAGCGCTCCGATCACTCGGCCACCGGATGGCGGCGCTTAAC 309
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 310 GGGCATCATCCCGTGACGTCTCTCGGTGACCTGGCAACCAAGTCGGGCGGACGCGT 369
QY 121 ThrGlyAsnValThrLeuAlaGlu 128
DB 370 ACAGGAGCGTGACATGGCCGAG 393

RESULT 28
US-09-620-412C-348
; Sequence 348, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-348

Alignment Scores:
Pred. No.: 6.9e-59 Length: 1464
Score: 608.00 Matches: 122
Percent Similarity: 96.09% Conservative: 1
Best Local Similarity: 95.31% Mismatches: 1
Query Match: 93.39% Indels: 4
DB: 4 Gaps: 1

US-09-684-215B-23 (1-128) x US-09-620-412C-348 (1-1464)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATTAATTCAGCTGTCACAGGTGGCAGGATTCGCCATTCCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
DB 82 GGGCAGCGCATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGTTTCAT 129
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAlaArg 60
DB 130 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTGTCGACACACACGCGGCGCAGCA 189
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Db 370 ACAGGAACGTGACATTGGCCGAG 393

RESULT 30

US-09-620-412C-332

; Sequence 332, Application US/09620412C

; Patent No. 6448234

; GENERAL INFORMATION:

; APPLICANT: Steven P. Fling

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469C7

; CURRENT APPLICATION NUMBER: US/09/620,412C

; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 363

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 332

; LENGTH: 1557

; TYPE: DNA

; ORGANISM: Chlamydia trachomatis

US-09-620-412C-332

Alignment Scores:

Pred. No.:	7,48e-59	Length:	1557
Score:	608.00	Matches:	122
Percent Similarity:	96.09%	Conservative:	1
Best Local Similarity:	95.31%	Mismatches:	4
Query Match:	93.39%	Indels:	4
DB:	4	Gaps:	1

US-09-684-215B-23 (1-128) x US-09-620-412C-332 (1-1557)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProle 20

Db 22 ACGCCCGCTCCGATAAATCCAGCTGTCAGAGGTGGCGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlySerProThrValHis 40

Db 82 GGGCAGCGATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGCTTCAAT 129

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60

Db 130 ATCGGCGCTACCGCTTCTCGGCTTGGTGTTCGACACAAACGGCAACGGCGACGA 189

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 190 GTCCAAACGGCTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 249

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

Db 250 ATACCGCGGTGACGGCGCTCCGATCACTCGGCCACCGCGATGGCGGCGGCTTAAC 309

Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyThrArg 120

Db 310 GGGCATCATCCCGTGCAGCTCATCTCGGTGACCTGGCAAAACCAAGTCGGCGCGACGCGT 369

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Db 370 ACAGGAACGTGACATTGGCCGAG 393

Search completed: April 30, 2004, 05:12:07

Job time : 713.531 secs

Db 370 ACAGGAACGTGACATTGGCCGAG 393

RESULT 29

US-09-598-419-348

; Sequence 348, Application US/09598419

; Patent No. 6565856

; GENERAL INFORMATION:

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Scholler, John

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469C6

; CURRENT APPLICATION NUMBER: US/09/598,419

; CURRENT FILING DATE: 2000-06-20

; NUMBER OF SEQ ID NOS: 357

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 348

; LENGTH: 1464

; TYPE: DNA

; ORGANISM: Chlamydia trachomatis

US-09-598-419-348

Alignment Scores:

Pred. No.:	6,9e-59	Length:	1464
Score:	608.00	Matches:	122
Percent Similarity:	96.09%	Conservative:	1
Best Local Similarity:	95.31%	Mismatches:	4
Query Match:	93.39%	Indels:	4
DB:	4	Gaps:	1

US-09-684-215B-23 (1-128) x US-09-598-419-348 (1-1464)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProle 20

Db 22 ACGCCCGCTCCGATAAATCCAGCTGTCAGAGGTGGCGAGGATTCGCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlySerProThrValHis 40

Db 82 GGGCAGCGATGGCGATCGCGGCCAGATCAAG-----CTTCCACCGCTTCAAT 129

Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60

Db 130 ATCGGCGCTACCGCTTCTCGGCTTGGTGTTCGACACAAACGGCAACGGCGACGA 189

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 190 GTCCAAACGGCTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTG 249

Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

Db 250 ATACCGCGGTGACGGCGCTCCGATCACTCGGCCACCGCGATGGCGGCGGCTTAAC 309

Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyThrArg 120

Db 310 GGGCATCATCCCGTGCAGCTCATCTCGGTGACCTGGCAAAACCAAGTCGGCGCGACGCGT 369

Qy 121 ThrGlyAsnValThrLeuAlaGlu 128

Search completed: April 30, 2004, 05:12:07

Job time : 713.531 secs

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Run on: April 29, 2004, 22:28:57 ; Search time 65.5311 seconds
(without alignments)
1083.969 Million cell updates/sec

Title: US-09-684-215B-18
Perfect score: 653
Sequence: 1 TAASDNFQSQSQGFAPL.....QTKSGGTRGNVLAEGPPA 128

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09684215@cgn_1_115 @runat_29042004_061306_13249 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCKS=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	653	100.0	675	4	US-09-636-215-822	Sequence 822, App
2	653	100.0	675	4	US-09-685-166A-822	Sequence 822, App
3	653	100.0	822	4	US-09-736-457-1862	Sequence 1862, App
4	653	100.0	900	4	US-09-643-597-353	Sequence 353, App
5	653	100.0	900	4	US-09-606-421B-353	Sequence 353, App
6	653	100.0	915	4	US-09-636-215-834	Sequence 834, App
7	653	100.0	915	4	US-09-685-166A-834	Sequence 834, App
8	653	100.0	945	4	US-09-736-457-1861	Sequence 1861, App
9	653	100.0	1012	4	US-09-643-597-351	Sequence 351, App
10	653	100.0	1012	4	US-09-606-421B-351	Sequence 351, App
11	653	100.0	1203	4	US-09-636-215-851	Sequence 851, App
12	653	100.0	1203	4	US-09-685-166A-851	Sequence 851, App

ALIGNMENTS

RESULT 1

US-09-636-215-822

; Sequence 822, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun C.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 822

; LENGTH: 675

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-636-215-822

Alignment Scores:

Pred. No.: 1.06e-67 Length: 675
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-685-166A-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGGTCCGATAAATTCAGCTGTCAGAGTGGCAGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGCGGCGAGATCAAGCTTCCACCGTTTATATCGGGCTTACC 141
QY 41 AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGGCTTGGGTGTTGTGACAAACACGCGCACGAGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGAGCGCTCCGCGGCAAGTCTCGCATCTCCACCGGCGAGTATACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAATCTCGGCCACCGGATGGCGGCGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCCGGCGGACCGGTACAGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGAGGAGACCCCGGCC 405

RESULT 3

US-09-736-457-1862
; Sequence 1862, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1862
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1862

Alignment Scores:
Pred. No.: 1.39e-67 Length: 822
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

Pred. No.: 1.06e-67 Length: 675
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-636-215-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGGTCCGATAAATTCAGCTGTCAGAGTGGCAGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGGCGATCGCGGCGAGATCAAGCTTCCACCGTTTATATCGGGCTTACC 141
QY 41 AlapheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCCTCGGCTTGGGTGTTGTGACAAACACGCGCACGAGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCCGAGCGCTCCGCGGCAAGTCTCGCATCTCCACCGGCGAGTATACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAATCTCGGCCACCGGATGGCGGCGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCTATCTCGGTGACCTGGCAACCAAGTCCGGCGGACCGGTACAGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGAGGAGACCCCGGCC 405

RESULT 2

US-09-685-166A-822
; Sequence 822, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-822

Alignment Scores:

QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCCACCGCGGACGTGATCACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAACTCGGCACCGCATGCGGACGCGTTTAAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGCGGCGACGCGTACGGGACGTCG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 6

US-09-636-215-834
; Sequence 834, Application US/09636215
; Patent No. 6620922

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 834
; LENGTH: 915

; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-636-215-834

Alignment Scores:
Pred. No.: 1,61e-67 Length: 915
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-636-215-834 (1-915)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATCAACTTCCAGCTGTCCAGGTTGGCGAGGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCTCGGCTTGGGTGTGTGTGTCGACACACACGCGACGCGGCGACGAGTCCACGCGTCG 201

QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
DB 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCCACCGCGGACGTGATCACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
DB 262 GACGGCGCTCCGATCAACTCGGCACCGCATGCGGACGCGTTTAAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArgThrGlyAsnVal 120
DB 322 GGTGACGTCACTCGGTGACCTGGCAACCAAGTCGGCGGCGACGCGTACGGGACGTCG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
DB 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 7

US-09-685-166A-834

; Sequence 834, Application US/09685166A

; Patent No. 6630385

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C21

; CURRENT APPLICATION NUMBER: US/09/685,166A

; CURRENT FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 898

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 834

; LENGTH: 915

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-685-166A-834

Alignment Scores:
Pred. No.: 1,61e-67 Length: 915
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-685-166A-834 (1-915)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATCAACTTCCAGCTGTCCAGGTTGGCGAGGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
DB 82 GGGCAGGCGATGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
DB 142 GCCTTCTCGGCTTGGGTGTGTGTGTCGACACACACGCGACGCGGCGACGAGTCCACGCGTCG 201

```
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGCGGCAAGTCTCGCATCTCCACCGGCGAGTGTATCATCCCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGGCGCTCCGATCAACTCGGCACCGCATGGCGGCGCGTTCACCGGCATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGTGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGCACGGGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGACCCCGGCC 405
RESULT 8
US-09-736-457-1861
; Sequence 1861, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1861
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1861
Alignment Scores:
Pred. No.: 1,69e-67 Length: 945
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-736-457-1861 (1-945)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCCGCTCCGATAAATCTTCCAGCTGCCAGGTCGGGAGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCATCGCGGCCAGATCAAGCTTCCACCGTTCATATCGGSCCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGCGACAAACACGCGCACGCGCAGTCCACACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGAGCGCTCCGGCGGCAAGTCTCGCATCTCCACCGCGACGTGATCACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCACCGCATGGCGGCGCGCTTAACGGGCATCATCCC 321
```

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QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGAGTGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGCACGGGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCCGAGGACCCCGGCC 405
RESULT 9
US-09-643-597-351
; Sequence 351, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 351
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-351
Alignment Scores:
Pred. No.: 1,85e-67 Length: 1012
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-643-597-351 (1-1012)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 67 ACGCCCGCTCCGATAAATCTTCCAGCTGCCAGGTCGGGAGGATTCGCCATTCGGATC 126
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 127 GGGCAGGCGATGGCATCGCGGCCAGATCAAGCTTCCACCGTTCATATCGGSCCTACC 186
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 187 GCCTTCCTCGCTTGGGTGTGTGCGACAAACACGCGCACGCGCAGTCCACACGCGTG 246
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 247 GTCGGAGCGCTCCGGCGGCAAGTCTCGCATCTCCACCGGCGACGTGATCACCGCGTC 306
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 307 GACGGCGCTCCGATCAACTCGGCACCGCATGGCGGCGCGCTTAACGGGCATCATCCC 366
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 367 GGTGAGTGTCATCTCGGTGACCTGGCAACCAAGTCGGCGGCGCACGGGTACAGGGAACGTG 426
QY 121 ThrLeuAlaGluGlyProProAla 128
```

Db 427 ACATTGGCGGAGGACCCCGGCGC 450

RESULT 10

US-09-606-421B-351

; Sequence 351, Application US/09606421B

; Patent No. 6531315

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606,421B

; CURRENT FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS: 358

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 351

; LENGTH: 1012

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-606-421B-351

Alignment Scores:

Pred. No.:	1,85e-67	Length:	1012
Score:	653.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-684-215B-18 (1-128) x US-09-606-421B-351 (1-1012)

QY	1	ThrAlaAlaSerAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle	20
DB	67	ACGGCGCGTCCGATTAACCTCCAGCTGCCAGGGTGGCAGGATTCGCCATTCGCATC	126
QY	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr	40
DB	127	GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCCTACC	186
QY	41	AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValArgValGlnArgVal	60
DB	187	GCCTTCTCGGCTTGGGTGTGTCGACAAACACGCGCACGAGTCCACGCGTG	246
QY	61	ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal	80
DB	247	GTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTGATCACCGCGTC	306
QY	81	AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro	100
DB	307	GACGGCGCTCCGATCAACTCGGCCACCGCATGGCGGACGCGCTTAACGGGCATCATCCC	366
QY	101	GlyAspValIleSerValThrTripglnThrLysSerGlyGlyThrArgThrGlyAsnVal	120
DB	367	GGTGACGTATCTCGGTGACCTGGCAACCAAGTCCGGCGGCACCGGTACAGGAACGTG	426
QY	121	ThrLeuAlaGluGlyProProAla	128
DB	427	ACATTGGCGGAGGACCCCGGCGC 450	

RESULT 11

US-09-636-215-851

; Sequence 851, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 851

; LENGTH: 1203

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-636-215-851

Alignment Scores:

Pred. No.:	2,34e-67	Length:	1203
Score:	653.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-684-215B-18 (1-128) x US-09-636-215-851 (1-1203)

QY	1	ThrAlaAlaSerAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle	20
DB	22	ACGGCGCGTCCGATTAACCTCCAGCTGCCAGGGTGGCAGGATTCGCCATTCGCATC	81
QY	21	GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr	40
DB	82	GGGCAGGCGATGGCGATCGCGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCCTACC	141
QY	41	AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValArgValGlnArgVal	60
DB	142	GCCTTCTCGGCTTGGGTGTGTCGACAAACACGCGCACGAGTCCACGCGTG	201
QY	61	ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal	80
DB	202	GTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGAGTGTATCACCGCGTC	261
QY	81	AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro	100
DB	262	GACGGCGCTCCGATCAACTCGGCCACCGCATGGCGGACGCGCTTAACGGGCATCATCCC	321
QY	101	GlyAspValIleSerValThrTripglnThrLysSerGlyGlyThrArgThrGlyAsnVal	120
DB	322	GGTGACGTATCTCGGTGACCTGGCAACCAAGTCCGGCGGCACCGGTACAGGAACGTG	381
QY	121	ThrLeuAlaGluGlyProProAla	128
DB	382	ACATTGGCGGAGGACCCCGGCGC 405	

RESULT 12

US-09-685-166A-851

; Sequence 851, Application US/09685166A

; Patent No. 5630305

; GENERAL INFORMATION:


```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-685-166A-851

Alignment Scores:
Pred. No.: 2,34e-67 Length: 1203
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-685-166A-851 (1-1203)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGCTCGATTAACCTTCAGCTGCCAGGGTGGGAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTTCGATTAACCTTCAGCTGCCAGGGTGGGAGGATTCGCCATTCGATC 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTGCGGAGCGCTTCGCGGCGCAAGTCTCGCATCTCCACGGCGAGCTGATCACCGCGTTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGCGCCACCGCGATGGCGGAGCGCTTAAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyThrArgThrGlyAsnVal 120
Db 322 GTGACGTCATCTCGGTGACCTGGCAACCAAGTCCGGCGGCACGCTACAGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGAGCCCCCGGCC 405

RESULT 13
US-09-620-412C-348
; Sequence 348, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scroller, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; US-09-598-419-348
Alignment Scores:

; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; US-09-620-412C-348

Alignment Scores:
Pred. No.: 3,07e-67 Length: 1464
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-620-412C-348 (1-1464)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGCTCGATTAACCTTCAGCTGCCAGGGTGGGAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTTCGATTAACCTTCAGCTGCCAGGGTGGGAGGATTCGCCATTCGATC 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTGCGGAGCGCTTCGCGGCGCAAGTCTCGCATCTCCACGGCGAGCTGATCACCGCGTTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGCGCCACCGCGATGGCGGAGCGCTTAAACGGGATCATCCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyThrArgThrGlyAsnVal 120
Db 322 GTGACGTCATCTCGGTGACCTGGCAACCAAGTCCGGCGGCACGCTACAGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGAGCCCCCGGCC 405

RESULT 14
US-09-598-419-348
; Sequence 348, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scroller, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; US-09-598-419-348
Alignment Scores:
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Pred. No.: 3,07e-67 Length: 1464
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-598-419-348 (1-1464)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGCGCTCCGATTAACCTTCCAGCTGTCCAGGGTGGGAGGAGTTCGCCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnLeuLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGGGGCCAGATCAAGCTTCCACCCTTCATATCGGGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGCGAACCAACGCAACGCGGCGAGTCCAGCTCCAGCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGGGCAAGTCTCGGCATCTCCACCGGGGACGTGATCACCGCGTTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCGATCAACTCGGCCACCGCATCGGCAGCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCGGTGACTGCGCAACCAAGTCCGGCGGCGACGGGTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGlyGlyProProAla 128
Db 382 ACATTCGCGGAGGAGGACCCCGGCC 405

RESULT 15

US-09-620-412C-332
; Sequence 332, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 332
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-332

Alignment Scores:
Pred. No.: 3,34e-67 Length: 1557
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-620-412C-332 (1-1557)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGCGCTCCGATTAACCTTCCAGCTGTCCAGGGTGGGAGGAGTTCGCCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnLeuLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGGGGCCAGATCAAGCTTCCACCCTTCATATCGGGCTACC 141

Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGCGAACCAACGCAACGCGGCGAGTCCAGCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGGGCAAGTCTCGGCATCTCCACCGGGGACGTGATCACCGCGTTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGCATCGGCAGCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCATCTCGGTGACCTGGCAACCAAGTCCGGCGGCGACGGGTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGlyGlyProProAla 128
Db 382 ACATTCGCGGAGGAGGACCCCGGCC 405

RESULT 16

US-09-598-419-332
; Sequence 332, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 332
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-332

Alignment Scores:
Pred. No.: 3,34e-67 Length: 1557
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-598-419-332 (1-1557)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGCGCTCCGATTAACCTTCCAGCTGTCCAGGGTGGGAGGAGTTCGCCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnLeuLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGGGGCCAGATCAAGCTTCCACCCTTCATATCGGGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGCGAACCAACGCAACGCGGCGAGTCCAGCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGGAGCGCTCCGGGGCAAGTCTCGGCATCTCCACCGGGGACGTGATCACCGCGTTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCAACTCGGCCACCGCATCGGCAGCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120

Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-598-419-188 (1-1578)
Qy 1 ThrAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGCCCGCTCCGATACCTTCCAGCTGTCAGGCGGAGATCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
Qy 41 AlapheLeuGlyLeuGlyValValAlaAspAenGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGACACAAACAGCGGCGGAGTCCAGCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACGGCGAGTGTATCACCGCGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCACTCACTCGGCCACCGCGATGGCGGACGGCTTAAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGGTGACCTGGCAACCAAGTCTGGCGGCGACCGGTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405
RESULT 21
US-09-598-419-352
; Sequence 352, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 352
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-352
Alignment Scores:
Pred. No.: 3,92e-67 Length: 1752
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-598-419-352 (1-1752)
Qy 1 ThrAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGCCCGCTCCGATACCTTCCAGCTGTCAGGCGGAGATCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
Qy 41 AlapheLeuGlyLeuGlyValValAlaAspAenGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGACACAAACAGCGGCGGAGTCCAGCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACGGCGAGTGTATCACCGCGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCACTCACTCGGCCACCGCGATGGCGGACGGCTTAAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGGTGACCTGGCAACCAAGTCTGGCGGCGACCGGTACAGGGAACGTG 381

Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-598-419-188 (1-1578)
Qy 1 ThrAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGCCCGCTCCGATACCTTCCAGCTGTCAGGCGGAGATCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
Qy 41 AlapheLeuGlyLeuGlyValValAlaAspAenGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGCTTGGGTGTGTGACACAAACAGCGGCGGAGTCCAGCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCCGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACGGCGAGTGTATCACCGCGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCACTCACTCGGCCACCGCGATGGCGGACGGCTTAAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTATCTCGGTGACCTGGCAACCAAGTCTGGCGGCGACCGGTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405
RESULT 20
US-09-620-412C-352
; Sequence 352, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 352
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-352
Alignment Scores:
Pred. No.: 3,92e-67 Length: 1752
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-620-412C-352 (1-1752)
Qy 1 ThrAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGCCCGCTCCGATACCTTCCAGCTGTCAGGCGGAGATCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGATGGCGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141

; CURRENT FILLING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-336
Alignment Scores:
Pred. No.: 3,94e-67 Length: 1758
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-598-419-336 (1-1758)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProle 20
Db 22 ACGGCGCGTCCGATAAATTCAGCTGCCAGGGTGGCAGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGCAGGGCGATCGGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGTTGGTGTGTCGACACACGACGCGGCGCAGGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACGGCGCGTATCACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCACTCGCCACCGGATGGCGGACGCGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCGGTGACCTGGCAACCAAGTCCGGCGGCGACGCGTACAGGACGCGT 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405
RESULT 24
US-09-620-412C-308
; Sequence 308, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILLING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 308
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-308
Alignment Scores:
Pred. No.: 4,25e-67 Length: 1860
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405
RESULT 22
US-09-620-412C-336
; Sequence 336, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILLING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-336
Alignment Scores:
Pred. No.: 3,94e-67 Length: 1758
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-684-215B-18 (1-128) x US-09-620-412C-336 (1-1758)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProle 20
Db 22 ACGGCGCGTCCGATAAATTCAGCTGCCAGGGTGGCAGGATTCGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGCAGGGCGATCGGATCGGGCCAGATCAAGCTTCCACCGTTTCATATCGGGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGTTGGTGTGTCGACACACGACGCGGCGCAGGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGGCGAGTATCACCGCGGTC 261
QY 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisPro 100
Db 262 GACGGCGCTCCGATCACTCGCCACCGGATGGCGGACGCGCTTAACGGGCATCATCC 321
QY 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCTCGGTGACCTGGCAACCAAGTCCGGCGGCGACGCGTACAGGACGCGT 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGAGGACCCCGGCC 405
RESULT 23
US-09-598-419-336
; Sequence 336, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419

US-09-684-215B-18 (1-128) x US-09-620-412C-308 (1-1860)

QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGGCGTCCGATTAATCTCCAGCTGTCCAGGGTGGCAGGATTCGCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTCAATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTTCGACAAACACGCAACGCGCAGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyLeuSerThrGlyAspValIleThrAlaVal 80
Db 322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCACGCGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 26
US-09-620-412C-324
; Sequence 324, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 324
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-324

Alignment Scores:
Pred. No.: 4,378-67 Length: 1896
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-620-412C-324 (1-1896)

QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGGCGTCCGATTAATCTCCAGCTGTCCAGGGTGGCAGGATTCGCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTCAATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTTCGACAAACACGCAACGCGCAGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyLeuSerThrGlyAspValIleThrAlaVal 80
Db 322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCACGCGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

US-09-684-215B-18 (1-128) x US-09-620-412C-308 (1-1860)

QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGGCGTCCGATTAATCTCCAGCTGTCCAGGGTGGCAGGATTCGCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTCAATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTTCGACAAACACGCAACGCGCAGTCCACGCGTG 201
QY 61 ValGlySerAlaProAlaAlaSerLeuGlyLeuSerThrGlyAspValIleThrAlaVal 80
Db 322 GGTGACGTCATCTCGGTGACCTGGCAACCAAGTCGGGCGGCACGCGTACAGGGAACGTG 381
QY 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 25
US-09-598-419-308
; Sequence 308, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 308
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-308

Alignment Scores:
Pred. No.: 4,256-67 Length: 1860
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-598-419-308 (1-1860)

QY 1 ThrAlaAlaSerAspAsnPhenLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGGCGTCCGATTAATCTCCAGCTGTCCAGGGTGGCAGGATTCGCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGGCGATGGCGATCGCGGCGCAGATCAAGCTTCCACCGTTCAATCGGCGCTACC 141
QY 41 AlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCTCGGCTTGGGTGTTCGACAAACACGCAACGCGCAGTCCACGCGTG 201

[illegible]

Db 22 ACAGCCCGCGTCCGATATCTCCAGCTGTCAGGGTGGGAGGATTCGCCATTCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGGATGGGATCGGGCCAGATCAAGCTTCCACCGTTCATATCGGGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTTGGGTGTGTTCGACAAACACGCGCACCGGACAGTCCAACCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGGAGCGATCCGGCGGCAAGTCTCGGCATCTCCACCGCGAGCTGATCACCGCGTC 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
Db 262 GACGGCGTCCGATCACTCGGCCACCGCGATGGCGGACGGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCATCTCGGTGACCTGCGCAACACCAAGTCGGCGGCGCACGCGTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

RESULT 30
US-09-620-412C-340
; Sequence 340, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 340
; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-340

Alignment Scores:
Pred. No.: 4.59e-67 Length: 1965
Score: 653.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-18 (1-128) x US-09-620-412C-340 (1-1965)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACAGCCCGCGTCCGATATCTCCAGCTGTCAGGGTGGGAGGATTCGCCATTCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40
Db 82 GGGCAGCGGATGGGATCGGGCCAGATCAAGCTTCCACCGTTCATATCGGGCTACC 141
Qy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60
Db 142 GCCTTCCTCGGCTTGGGTGTGTTCGACAAACACGCGCACCGGACAGTCCAACCGGTG 201
Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80
Db 202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGACGTGATCACCGGTG 261
Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100

Db 262 GACGGCGTCCGATCACTCGGCCACCGCGATGGCGGACCGCTTAACGGGCATCATCCC 321
Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
Db 322 GGTGACGTCATCTCGGTGACCTGCGCAACACCAAGTCGGCGGCGCACGCTACAGGGAACGTG 381
Qy 121 ThrLeuAlaGluGlyProProAla 128
Db 382 ACATTGGCGGAGGACCCCGGCC 405

Search completed: April 30, 2004, 05:01:19
Job time : 76.5311 secs

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OM protein - protein search, using sw model

Run on: April 20, 2004, 06:21:52 ; Search time 22 Seconds
(without alignments)
300.369 Million cell updates/sec

Title: US-09-684-215B-18

Perfect score: 653

Sequence: 1 TAASDNFQLSQGGQGAIPA.....QTKSGGTRGNVTLAEGPPA 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	653	100.0	224	4	US-09-636-215-825
2	653	100.0	224	4	US-09-685-166A-825
3	653	100.0	267	4	US-09-643-597-352
4	653	100.0	267	4	US-09-608-421B-352
5	653	100.0	273	4	US-09-736-457-1864
6	653	100.0	299	4	US-09-643-597-354
7	653	100.0	299	4	US-09-606-421B-354
8	653	100.0	304	4	US-09-636-215-835
9	653	100.0	304	4	US-09-685-166A-835
10	653	100.0	314	4	US-09-736-457-1863
11	653	100.0	400	4	US-09-636-215-852
12	653	100.0	400	4	US-09-685-166A-852
13	653	100.0	487	4	US-09-620-412C-349
14	653	100.0	487	4	US-09-598-419-349
15	653	100.0	518	4	US-09-620-412C-333
16	653	100.0	518	4	US-09-598-419-333
17	653	100.0	525	4	US-09-556-877-196
18	653	100.0	525	4	US-09-620-412C-196
19	653	100.0	525	4	US-09-598-419-196
20	653	100.0	583	4	US-09-620-412C-353
21	653	100.0	583	4	US-09-598-419-353
22	653	100.0	585	4	US-09-620-412C-337
23	653	100.0	585	4	US-09-598-419-337
24	653	100.0	619	4	US-09-620-412C-309
25	653	100.0	619	4	US-09-598-419-309
26	653	100.0	631	4	US-09-620-412C-325
27	653	100.0	631	4	US-09-598-419-325

Sequence 317, App
Sequence 317, App
Sequence 341, App
Sequence 341, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 313, App
Sequence 313, App
Sequence 313, App
Sequence 345, App
Sequence 345, App
Sequence 321, App
Sequence 321, App
Sequence 329, App
Sequence 329, App
Sequence 329, App
Sequence 28, Appli
Sequence 2, Appli
Sequence 66, Appli

28 653 100.0 646 4 US-09-620-412C-317
29 653 100.0 646 4 US-09-598-419-317
30 653 100.0 654 4 US-09-620-412C-341
31 653 100.0 654 4 US-09-598-419-341
32 653 100.0 683 4 US-09-620-412C-357
33 653 100.0 683 4 US-09-598-419-357
34 653 100.0 691 4 US-09-620-412C-313
35 653 100.0 691 4 US-09-598-419-313
36 653 100.0 700 4 US-09-620-412C-345
37 653 100.0 700 4 US-09-598-419-345
38 653 100.0 715 4 US-09-620-412C-321
39 653 100.0 715 4 US-09-620-412C-329
40 653 100.0 715 4 US-09-598-419-329
41 653 100.0 715 4 US-09-598-419-329
42 632 96.8 231 4 US-09-287-849-28
43 632 96.8 729 4 US-09-223-040-2
44 632 96.8 729 4 US-09-287-849-2
45 627 96.0 132 3 US-08-818-112-66

ALIGNMENTS

RESULT 1
US-09-636-215-825
; Sequence 825, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 825

; LENGTH: 224

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-636-215-825

Query Match 100.0%; Score 653; DB 4; Length 224;
Best local Similarity 100.0%; Pred. No. 1e-67; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0;

QY 1 TAASDNFQLSQGGQGAIPAIGQAMAIAGQIKLPTVHIGFTAFGLGVNDNNGARVQRV 60

DB 8 TAASDNFQLSQGGQGAIPAIGQAMAIAGQIKLPTVHIGFTAFGLGVNDNNGARVQRV 67

QY 61 VGSAPASLGISTGVDVITAVDGPINSATAMADALNHHPGDVISTVWTKSGGTGTGNV 120

DB 68 VGSAPASLGISTGVDVITAVDGPINSATAMADALNHHPGDVISTVWTKSGGTGTGNV 127

QY 121 TLAEGPPA 128

DB 128 TLAEGPPA 135

; CURRENT APPLICATION NUMBER: US/09/643,597
 ; CURRENT FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 369
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 352
 ; LENGTH: 267
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-643-597-352

Query Match 100.0%; Score 653; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.3e-67;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TAASDNFOLSGGGGFAIPIGQMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV	60
DB	8	TAASDNFOLSGGGGFAIPIGQMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV	67
QY	61	VGSAPAAASLGISTGDIVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV	120
DB	68	VGSAPAAASLGISTGDIVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV	127
QY	121	TLAEGPPA 128	
DB	128	TLAEGPPA 135	

RESULT 4
 US-09-606-421B-352
 ; Sequence 352, Application US/09606421B
 ; Patent No. 6531315
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C9
 ; CURRENT APPLICATION NUMBER: US/09/606,421B
 ; CURRENT FILING DATE: 2000-06-28
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 352
 ; LENGTH: 267
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-606-421B-352

Query Match 100.0%; Score 653; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.3e-67;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TAASDNFOLSGGGGFAIPIGQMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV	60
DB	8	TAASDNFOLSGGGGFAIPIGQMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV	67
QY	61	VGSAPAAASLGISTGDIVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV	120
DB	68	VGSAPAAASLGISTGDIVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV	127
QY	121	TLAEGPPA 128	
DB	128	TLAEGPPA 135	

RESULT 5
 US-09-736-457-1864

RESULT 2
 US-09-685-166A-825
 ; Sequence 825, Application US/09685166A
 ; Patent No. 6630305
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Barrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C21
 ; CURRENT APPLICATION NUMBER: US/09/685,166A
 ; CURRENT FILING DATE: 2000-10-10
 ; NUMBER OF SEQ ID NOS: 898
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 825
 ; LENGTH: 224
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-685-166A-825

Query Match 100.0%; Score 653; DB 4; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1e-67;
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TAASDNFOLSGGGGFAIPIGQMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV	60
DB	8	TAASDNFOLSGGGGFAIPIGQMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV	67
QY	61	VGSAPAAASLGISTGDIVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV	120
DB	68	VGSAPAAASLGISTGDIVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV	127
QY	121	TLAEGPPA 128	
DB	128	TLAEGPPA 135	

RESULT 3
 US-09-643-597-352
 ; Sequence 352, Application US/09643597
 ; Patent No. 6426072
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C11

; Sequence 1864, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriek
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C13
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1864
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1864

Query Match 100.0%; Score 653; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFOLSQGGGFAIPIGQAMAIAQIKLPTVHIGTAFGLGVVDNNGNGARVORV 60
DB 8 TAASDNFOLSQGGGFAIPIGQAMAIAQIKLPTVHIGTAFGLGVVDNNGNGARVORV 67

QY 61 VGSAPAAASLGISTGDTAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 127

QY 121 TLAEGP 128
DB 128 TLAEGP 135

RESULT 6
US-09-643-597-354
; Sequence 354, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-354

Query Match 100.0%; Score 653; DB 4; Length 299;

Best Local Similarity 100.0%; Pred. No. 1.5e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFOLSQGGGFAIPIGQAMAIAQIKLPTVHIGTAFGLGVVDNNGNGARVORV 60
DB 8 TAASDNFOLSQGGGFAIPIGQAMAIAQIKLPTVHIGTAFGLGVVDNNGNGARVORV 67

QY 61 VGSAPAAASLGISTGDTAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 127

QY 121 TLAEGP 128
DB 128 TLAEGP 135

RESULT 7
US-09-606-421B-354
; Sequence 354, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-354

Query Match 100.0%; Score 653; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.5e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFOLSQGGGFAIPIGQAMAIAQIKLPTVHIGTAFGLGVVDNNGNGARVORV 60
DB 8 TAASDNFOLSQGGGFAIPIGQAMAIAQIKLPTVHIGTAFGLGVVDNNGNGARVORV 67

QY 61 VGSAPAAASLGISTGDTAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 127

QY 121 TLAEGP 128
DB 128 TLAEGP 135

RESULT 8
US-09-636-215-835
; Sequence 835, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 835
LENGTH: 304
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-215-835

Query Match 100.0%; Score 653; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 9
US-09-685-166A-835
Sequence 835, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 835
LENGTH: 304
TYPE: PRT
ORGANISM: Homo sapiens
US-09-685-166A-835

Query Match 100.0%; Score 653; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 10
US-09-736-457-1863
Sequence 1863, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Lijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1863
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-09-736-457-1863

Query Match 100.0%; Score 653; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 11
US-09-636-215-852
Sequence 852, Application US/09636215
Patent No. 6620322
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui

```
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-852

Query Match      100.0%; Score 653; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db      8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY      61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
Db      68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY      121 TLAEGPPA 128
Db      128 TLAEGPPA 135

RESULT 13
US-09-620-412C-349
; Sequence 349, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 349
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-349

Query Match      100.0%; Score 653; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db      8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY      61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
Db      68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY      121 TLAEGPPA 128
Db      128 TLAEGPPA 135

RESULT 14
US-09-598-419-349
; Sequence 349, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 349
; LENGTH: 487
```

```
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-852

Query Match      100.0%; Score 653; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db      8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY      61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
Db      68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY      121 TLAEGPPA 128
Db      128 TLAEGPPA 135

RESULT 12
US-09-685-166A-852
; Sequence 852, Application US/09685166A
; Patent No. 5630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 852
; LENGTH: 400
```

```
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-333

Query Match      100.0%; Score 653; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 17
US-09-556-877-196
; Sequence 196, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556.877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 196
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-196

Query Match      100.0%; Score 653; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 3.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 18
US-09-620-412C-196
; Sequence 196, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 196
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-333

Query Match      100.0%; Score 653; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 15
US-09-620-412C-333
; Sequence 333, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 333
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-333

Query Match      100.0%; Score 653; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 3.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHPGDVSVTWQTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 16
US-09-598-419-333
; Sequence 333, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 333
; LENGTH: 518
```

SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 353
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-353

Query Match 100.0%; Score 653; DB 4; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.9e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 21
US-09-598-419-353
; Sequence 353, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 353
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-353

Query Match 100.0%; Score 653; DB 4; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.9e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 22
US-09-620-412C-337
; Sequence 337, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 196
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-196

Query Match 100.0%; Score 653; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 3.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 19
US-09-598-419-196
; Sequence 196, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 196
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-598-419-196

Query Match 100.0%; Score 653; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 3.4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67
QY 61 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGVDVITAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 20
US-09-620-412C-353
; Sequence 353, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363

```

; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 309
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-309

Query Match      100.0%; Score 653; DB 4; Length 619;
Best Local Similarity 100.0%; Pred. No. 4.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 25
US-09-598-419-309
; Sequence 309, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 309
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-309

Query Match      100.0%; Score 653; DB 4; Length 619;
Best Local Similarity 100.0%; Pred. No. 4.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 26
US-09-620-412C-325
; Sequence 325, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
```

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; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 337
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-337

Query Match      100.0%; Score 653; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 23
US-09-598-419-337
; Sequence 337, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 337
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-337

Query Match      100.0%; Score 653; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 4e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
Db 128 TLAEGPPA 135

RESULT 24
US-09-620-412C-309
; Sequence 309, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
```


SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 317
LENGTH: 646
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-317

Query Match 100.0%; Score 653; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 4.6e-67; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 29
US-09-598-419-317
Sequence 317, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 317
LENGTH: 646
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-598-419-317

Query Match 100.0%; Score 653; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 4.6e-67; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 30
US-09-620-412C-341
Sequence 341, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 325
LENGTH: 631
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-325

Query Match 100.0%; Score 653; DB 4; Length 631;
Best Local Similarity 100.0%; Pred. No. 4.4e-67; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 27
US-09-598-419-325
Sequence 325, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 325
LENGTH: 631
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-598-419-325

Query Match 100.0%; Score 653; DB 4; Length 631;
Best Local Similarity 100.0%; Pred. No. 4.4e-67; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVQRV 67

QY 61 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGAPINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV 127

QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 28
US-09-620-412C-317
Sequence 317, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 357
LENGTH: 683
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-357

Query Match 100.0%; Score 653; DB 4; Length 683;
Best Local Similarity 100.0%; Pred. No. 4.9e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 33
US-09-598-419-357
Sequence 357, Application US/09598419
Patent No. 8565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 357
LENGTH: 683
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-598-419-357

Query Match 100.0%; Score 653; DB 4; Length 683;
Best Local Similarity 100.0%; Pred. No. 4.9e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 34
US-09-620-412C-313
Sequence 313, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 341
LENGTH: 654
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-620-412C-341

Query Match 100.0%; Score 653; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 4.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 31
US-09-598-419-341
Sequence 341, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 341
LENGTH: 654
TYPE: PRT
ORGANISM: Chlamydia trachomatis
US-09-598-419-341

Query Match 100.0%; Score 653; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 4.6e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 60
DB 8 TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGPTAFGLGVVDNNGGARVQRV 67
QY 61 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 120
DB 68 VGSAPAAASLGISTGDTVITAVDGPINSATAMADALNGHHHPGDVSVTWTKSGGTRTGNV 127
QY 121 TLAEGPPA 128
DB 128 TLAEGPPA 135

RESULT 32
US-09-620-412C-357
Sequence 357, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363

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; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 345
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-145

```

Query Match	100.0%;	Score 653;	DB 4;	Length 700;
Best Local Similarity	100.0%;	Pred. No. 5.1e-67;		
Matches 128;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGFTAFGLGVVDNNGCARVQRV	60	
DB	8	TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVHIGFTAFGLGVVDNNGCARVQRV	67	
QY	61	VGSAPASLSIGISTGDIIVTAVDGA PINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV	120	
DB	68	VGSAPASLSIGISTGDIIVTAVDGA PINSATAMADALNGHHPGDVISVTWTKSGGTRTGNV	127	
QY	121	TLAEGPPA	128	
DB	128	TLAEGPPA	135	

```

RESULT 37
US-09-598-419-345
; Sequence 345, Application US/09598419
; Patent NO. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Schoeller, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 345
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-345

```

Query Match	100.0%;	Score 653;	DB 4;	Length 700;
Best Local Similarity	100.0%;	Pred. No. 5.1e-67;		
Matches 128;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVTHIGTPTAFLGLGVVDNNGGARVQV	60	
Db	8	TAASDNFQLSQGGGFAIPIGQAMATAGQIKLPTVTHIGTPTAFLGLGVVDNNGGARVQV	67	
QY	61	VGSAPASLSIGITGDVITAVDGPAINSATAMADALNGHPGDVSVTWTKSGGTRIGNV	120	
Db	68	VGSAPASLSIGITGDVITAVDGPAINSATAMADALNGHPGDVSVTWTKSGGTRIGNV	127	
QY	121	TLAEGPPA	128	
Db	128	TLAEGPPA	135	

RESULT 38
US-09-620-412C-321
; Sequence 321, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363

; SOFTWARE: Fast-SEQ for Windows Version 3.0/4.0
; SEQ ID NO 321
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-321

Query Match 100.0%; Score 653; DB 4; Length 715;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
Qy 61 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
Qy 121 TLAEPPA 128
Db 128 TLAEPPA 135

RESULT 41
US-09-598-419-329
; Sequence 329, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: Fast-SEQ for Windows Version 3.0/4.0
; SEQ ID NO 329
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-598-419-329

Query Match 100.0%; Score 653; DB 4; Length 715;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
Qy 61 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
Qy 121 TLAEPPA 128
Db 128 TLAEPPA 135

Search completed: April 20, 2004, 06:25:00
Job time : 23 secs

; SOFTWARE: Fast-SEQ for Windows Version 3.0/4.0
; SEQ ID NO 321
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-321

Query Match 100.0%; Score 653; DB 4; Length 715;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 60
Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
Qy 61 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
Qy 121 TLAEPPA 128
Db 128 TLAEPPA 135

RESULT 39
US-09-620-412C-329
; Sequence 329, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: Fast-SEQ for Windows Version 3.0/4.0
; SEQ ID NO 329
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-329

Query Match 100.0%; Score 653; DB 4; Length 715;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 8 TAASDNFQLSQGGGFAIPIGQAMAIAGQIKLPTVHIGPTAFGLGVVDNNGNGARVORV 67
Qy 61 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 120
Db 68 VGSAPAAASLGISTGDIVTAVDGPINSATAMADALNGHHHPGDVISVTWTKSGGTRTGNV 127
Qy 121 TLAEPPA 128
Db 128 TLAEPPA 135

RESULT 40
US-09-598-419-321
; Sequence 321, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 20:32:52 ; Search time 3784.74 Seconds

(without alignments)
1511.672 Million cell updates/sec

Title: US-09-684-215B-4

Perfect score: 675

Sequence: 1 TAASDNFQLSQGGQGFAPLPI.....QTKSGGTRTGNVTLAAGPPA 132

Scoring table: BLOSUM62

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Ygapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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39: em.htgo.hum.*
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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	675	100.0	702	6	BD251334 Fused pro
2	675	100.0	702	6	AR403747 Sequence
3	675	100.0	1068	6	BD274032 Sequence
4	675	100.0	1068	6	AX005788 Sequence
5	675	100.0	1143	6	BD274033 Sequence
6	675	100.0	1143	6	AX005790 Sequence
7	675	100.0	2287	6	BD251322 Fused pro
8	675	100.0	2287	6	AR303127 Sequence
9	675	100.0	2287	6	AR403735 Sequence
10	675	100.0	14029	1	AE006925 Mycobacte
11	675	100.0	341957	15	BX842572 Mycobacte
12	675	100.0	343050	1	BX248334 Mycobacte
13	670	99.3	447	6	AR169152 Sequence
14	670	99.3	447	6	AR182442 Sequence
15	670	99.3	447	6	AR194825 Sequence
16	670	99.3	447	6	AR233097 Sequence
17	670	99.3	447	6	AR353302 Sequence
18	670	99.3	447	6	AX429596 Sequence
19	670	99.3	447	6	AX832581 Sequence
20	670	99.3	447	6	BD006325 Compounds
21	670	99.3	447	6	BD006445 Compounds
22	670	99.3	447	6	BD069285 Compounds
23	670	99.3	447	6	BD205817 Compounds
24	670	99.3	1872	6	AR169165 Sequence
25	670	99.3	1872	6	AR182455 Sequence
26	670	99.3	1872	6	AR194838 Sequence
27	670	99.3	1872	6	AR233110 Sequence
28	670	99.3	1872	6	AR353315 Sequence
29	670	99.3	1872	6	AX429609 Sequence
30	670	99.3	1872	6	AX832594 Sequence
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32	670	99.3	1872	6	BD006458 Compounds
33	670	99.3	1872	6	BD069298 Compounds
34	670	99.3	1872	6	BD205830 Compounds
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36	632	93.6	675	6	AR400535 Sequence
37	632	93.6	675	6	AR405802 Sequence
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42	632	93.6	894	6	AX351489 Sequence
43	632	93.6	900	6	AR220690 Sequence
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ALIGNMENTS

RESULT 1

BD251334 702 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Fused protein of Mycobacterium tuberculosis antigen and utilization thereof.
ACCESSION BD251334 GI:33061104
VERSION BD251334.1
KEYWORDS JP 2002510494-A/13.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 702)
AUTHORS Skeiky, Y.A.W., Alderson, M. and Neto, A.C.
TITLE Fused protein of Mycobacterium tuberculosis antigen and utilization thereof
JOURNAL Patent: JP 2002510494-A 13 09-APR-2002;
CORIXA CORP
COMMENT OS Artificial Sequence
PN JP 2002510494-A/13
PD 09-APR-2002
PF 07-APR-1999 JP 2000542460
PR 07-APR-1998 US 09/056556, 30-DEC-1998 US 09/223040 PI
YASIR A W SKEIKY, MARK ALDERSON, ANTONIO CAMPOS NETO PC
C12N15/09, A61K39/04, A61K48/00, A61P31/04, C07K14/35, C07K19/00, PC
C12P21/02.
PC C12N15/00
CC Description of Artificial Sequence: bi-fusion
protein Ral2-DPPD
CC (designated
CC Mt24), reading frame 1
CC bi-fusion protein Ral2-DPPD (designated Mt24), reading frame 1
CC reading frame 2
CC reading frame 3
FH key Location/Qualifiers
FT CDS (1)..(696)
FT CDS (2)..(700)
FT CDS (3)..(701).
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source
1. 702
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/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 2.37e-42 Length: 702
Score: 675.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 25 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGGTGGGAGGATTCGCCATTCGGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCA 144
QY 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyAsnGlyAlaArg 60
DB 145 ATCGGGCTTACCGCTTCTCGGCTTGGTGTTCGACAAACACGGCAACGGCGACGA 204
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 205 GTCCACCGCGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 265 ATCACCGCGTGGCGGCGCTCCGATCACTCGGCCACCGCGATGGCGACGCGTTAAC 324
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTCGCAACCAACCAAGTCGGCGCGCGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
DB 385 ACAGGAACGTGACATTGGCCGAGGACCCCGGCC 420
RESULT 3
BD274032 1068 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequences nucleic acid from polypeptides exportes from mycobacteries, vector the complement and applications at diagnostic and the prevention from the tuberculosis.

QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAACCAACCAAGTCGGCGCGCGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
DB 385 ACAGGAACGTGACATTGGCCGAGGACCCCGGCC 420
RESULT 2
AR403747 702 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 27 from patent US 6627198.
ACCESSION AR403747
VERSION AR403747.1 GI:40151423
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 702)
AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Alderson, M. and Campos-Neto, A.
TITLE Fusion proteins of Mycobacterium tuberculosis antigens and their uses
JOURNAL Patent: US 6627198-A 27 30-SEP-2003;
FEATURES Location/Qualifiers
1. 702
/organism="unknown"
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Pred. No.: 2.37e-42 Length: 702
Score: 675.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 25 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGGTGGGAGGATTCGCCATTCGGATC 84
QY 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 85 GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCA 144
QY 41 IleGlyProThrAlaPheLeuGlyValValAlaAspAsnGlyAsnGlyAlaArg 60
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QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 205 GTCCACCGCGTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 264
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 265 ATCACCGCGTGGCGGCGCTCCGATCACTCGGCCACCGCGATGGCGACGCGTTAAC 324
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
DB 325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTCGCAACCAACCAAGTCGGCGCGCGCGT 384
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
DB 385 ACAGGAACGTGACATTGGCCGAGGACCCCGGCC 420
RESULT 3
BD274032 1068 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequences nucleic acid from polypeptides exportes from mycobacteries, vector the complement and applications at diagnostic and the prevention from the tuberculosis.

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ACCESSION BD274032
VERSION BD274032.1 GI:33083800
KEYWORDS JP 2002534956-A/256.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Gicquel, B., Portnoi, D., Lim, E., Pellicic, V., Guigueno, A. and
Salmoniere, Y.G.D.L.
TITLE Sequences nucleic acid from polypeptides exportes from
mycobacteries, vector the complement and applications at diagnostic
and the prevention from the tuberculose
JOURNAL Patent: JP 2002534956-A 256 22-OCT-2002;
INSTITUT PASTEUR
COMMENT CS Mycobacterium tuberculosis
PN JP 2002534956-A/256
PD 22-OCT-2002
PF 14-AUG-1998 JP 2000509849
PR 14-AUG-1997 FR 97/10404, 11-SEP-1997 FR 97/11325 PI
BRIGITTE GICQUEL, DENIS PORTNOI, ENG-MONG LIM, VLADIMIR PELICIC, PI
AGNES GUIGUENO, YVES GOGUET DE LA SALMONIERE
PC C12N15/09, A61K39/00, A61K48/00, A61P11/00, A61P31/04, C07K14/35,
C07K16/12, C07K19/00, C12N1/21, C12P21/02, C12Q1/02, C12Q1/68, G01N33/50, PC
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Pred. No.: 3 59e-42 Length: 1068
Score: 675.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 730 GGGCAGCGGATGGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCAACCCCGTTTCA 789
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
Db 790 ATCGGGCTACCGCTTCTCCGGTGGTGTTCGACAAACACGCGACGCGCAGCA 849
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 850 GTCCACCGGTGGTGGGAGCGCTCCGCGCGAGTCTCGGCATCTCCACCGCGCAGTG 909
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 910 ATCACC CGGTTCGACGCGCTCCGATCAACTCCACCGCATCTCCACCGCGCTAAC 969
QY 101 GlyHisHisProGlyAspValIleSerValThrGlnThrIleHisSerGlyGlyThrArg 120
Db 970 GGGCATCATCCGCTGACGTCATCTCGGTGACCTTGGCAACCAAGTCCGCGCGCA 1029
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

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Db 925 GTTCAACGGGTGGTGGGAGCGCTCGGGGCGAAGTCTCGGCATCTCCACCGCGCGGTG 984
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 Db 985 ATCAGCGCGTGCAGCGCGCTCCGATCACTCGGCACCGCATGGCGGACGCGCTTAAC 1044
 QY 101 GlyHisHieProGlyAspValIleSerValThrTpGlnThrIleValSerGlyGlyThrArg 120
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 QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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 DEFINITION Sequence 909 from Patent WO9909186.
 ACCESSION AX005790
 VERSION AX005790.1 GI:9928797
 KEYWORDS
 SOURCE Mycobacterium tuberculosis
 ORGANISM Mycobacterium tuberculosis
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 REFERENCE 1
 AUTHORS Portnoi, D. and Guigueno, A.
 TITLE Polypeptide nucleic sequences exported from mycobacteria, vectors
 comprising same and uses for diagnosing and preventing tuberculosis
 JOURNAL Patent: WO 9909186-A 309 25-FEB-1999;
 PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
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 ORIGIN
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 Score: 675.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 US-09-684-215B-4 (1-132) x AX005790 (1-1143)
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 Db 745 ACGCGCGGTCCGATAACTTCAGCTGTCCAGGTCGGCAGGATTCGCCATTCGGATC 804
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
 Db 805 GGGCAGGCGATCGCATCGCGGCGCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCA 864
 QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAsnGlyAlaArg 60

Db 970 GGGCATATCCCGGTGAGCGTCACTCGGTGACCTGGGCAAAACCAAGTCGGCGGCGCACCGGT 1029
 QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
 Db 1030 ACAGGGAACGTGACATTGGCGGAGGAGCCCGCGCC 1065
 RESULT 5
 BD274033 1143 bp DNA linear PAT 17-JUL-2003
 LOCUS BD274033 1143 bp DNA linear PAT 17-JUL-2003
 DEFINITION Sequences nucleic acid from polypeptides exportes from
 mycobacteries, vector the complement and applications at diagnostic
 and the prevention from the tuberculose.
 ACCESSION BD274033 GI:33083801
 VERSION BD274033.1
 KEYWORDS Mycobacterium tuberculosis
 SOURCE Mycobacterium tuberculosis
 ORGANISM Mycobacterium tuberculosis
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 REFERENCE 1 (bases 1 to 1143)
 AUTHORS Gicquel, B., Portnoi, D., Lim, E., Pellicic, V., Guigueno, A. and
 Salmoniere, Y. G. D. B.
 TITLE Sequences nucleic acid from polypeptides exportes from
 mycobacteries, vector the complement and applications at diagnostic
 and the prevention from the tuberculose
 JOURNAL Patent: JP 2002534956-A 257 22-OCT-2002;
 INSTITUT PASTEUR
 COMMENT OS Mycobacterium tuberculosis
 PN JP 2002534956-A/257
 PD 22-OCT-2002
 PF 14-AUG-1998 JP 2000509849
 PR 14-AUG-1997 FR 97/10404, 11-SEP-1997 FR 97/11325 PI
 BRIGITTE GICQUEL, DENIS PORTNOI, ENG-MONG LIM, VLADIMIR PELICIC, PI
 AGNES GUIGUENO, YVES GOGUET DE LA SALMONIERE
 PC C12N15/09, A61K39/04, A61K48/00, A61P11/00, A61P31/04, C07K14/35,
 C07K16/12,
 PC C07K19/00, C12N1/21, C12P21/02, C12Q1/02, C12Q1/68, G01N33/50, PC
 G01N33/53//
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 FH Key Location/Qualifiers
 FT CDS (4)..(1140).
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 /db_xref="taxon:1773"
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 Pred. No.: 3.85e-42 Length: 1143
 Score: 675.00 Matches: 132
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 Db 745 ACGCGCGGTCCGATAACTTCAGCTGTCCAGGTCGGCAGGATTCGCCATTCGGATC 804
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
 Db 805 GGGCAGGCGATCGCATCGCGGCGCAGATCCGATCGGGTGGGGGTCAACCCACCGTTTCA 864
 QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAsnGlyAlaArg 60
 Db 865 ATCGGCGCTACCGCTTCTCGGCTTGGTGTGTTCGACACCAACGCGCACGGCGCACGA 924
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 865 ATCGGCGCTACCGCTTCTCGGCTTGGTGTTCGACAAACGGCAACGGCGCACGA 924
 QY 61 ValGlnArgValValGlySerAlaProAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 925 GTTCAACGGGTGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCGGTG 984
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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 Db 1045 GGGCATCATCCCGGTGACGTCTCGGTGACCTGGCAACCAAGTCCGGCGGCGCACGCT 1104
 QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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RESULT 7
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 LOCUS
 DEFINITION Fused protein of Mycobacterium tuberculosis antigen and utilization thereof.
 ACCESSION BD251322.1 GI:33061092
 VERSION BD251322.1
 KEYWORDS JP 2002510494-A/1.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 1 (bases 1 to 2287)
 REFERENCE 1 (bases 1 to 2287)
 AUTHORS Skeiky, Y.A.W., Alderson, M. and Neto, A.C.
 TITLE Fused protein of Mycobacterium tuberculosis antigen and utilization thereof
 JOURNAL Patent: JP 2002510494-A 1 09-APR-2002;
 CORIXA CORP
 COMMENT OS Artificial Sequence
 FN JP 2002510494-A/1
 PD 09-APR-2002
 PR 07-APR-1998 JP 2000542460
 PR 07-APR-1998 US 09/565556; 30-DEC-1998 US 09/223040 PI
 YASIR A W SKEIKY, MARK ALDERSON, ANTONIO CAMPOS NETO PC
 C12N15/09, A61K39/04, A61K48/00, A61P31/04, C07K14/35, C07K19/00, PC
 C12P21/02.
 PC C12N15/00
 CC Description of Artificial Sequence: tri-fusion protein Ral2- CC
 TbH9-Ra35
 CC (designated Mtb32A)
 CC n = g, a, c o r t
 CC n = g, a, c o r t
 CC n = g, a, c o r t
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 FT CDS (42)... (2231)
 FT modified_base (2270).
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Alignment Scores:
 Pred. No.: 7.67e-42 Length: 2287
 Score: 675.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-684-215B-4 (1-132) x BD251322 (1-2287)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
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 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyIleSerProThrValHis 40
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 Db 193 ATCGGGCGTACCGGCTTCTCGGCTTGGGTGTTCGACAAACGGCAACGGCGCACGA 242
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 243 GTTCAACGGGTGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGCGGTG 302
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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 QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyIleThrArg 120
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 QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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RESULT 8
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 LOCUS
 DEFINITION Sequence 1 from patent US 6544522.
 ACCESSION AR303127
 VERSION AR303127.1 GI:31691855
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 2287)
 REFERENCE 1 (bases 1 to 2287)
 AUTHORS Skeiky, Y., Alderson, M. and Campos-Neto, A.
 TITLE Fusion proteins of mycobacterium tuberculosis antigens and their uses
 JOURNAL Patent: US 6544522-A 1 08-APR-2003;
 FEATURES Location/Qualifiers
 source 1..2287
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 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 7.67e-42 Length: 2287
 Score: 675.00 Matches: 132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-684-215B-4 (1-132) x AR303127 (1-2287)

QY 1 ThrAlaAlaSerAspAsnPhenGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
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 Db 123 GGGCAGCGCATGGCGATCGCGGGCCAGATCCGATCCGCTGGGGGTACCCACCGTTCAT 182
 QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
 Db 183 ATCGGGCGTACCGGCTTCTCGGCTTGGGTGTTCGACAAACGGCAACGGCGCACGA 242
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 243 GTCCAAACGGTGGTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTG 302

Qy 81 HleThraValAspGlyValAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

Db 303 ATCACCAGCGTCCGAGCGCTCCGATCACTCCGCCACCGGATCGCGAGCGCGCTTAAC 362

Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

Db 363 GGGCATCATCCCGGTGACGTCTCGGTGACCTCGCAACCAAGTCGGGGCGGACGCGT 422

Qy 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

Db 423 ACAGGAACGTGACATTGGCCGAGGACCCCGGCC 458

RESULT 9

AR403735

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 2287)

Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.

AUTHORS

Fusion proteins of Mycobacterium tuberculosis antigens and their

TITLE

uses

Patent: US 6627198-A 1 30-SEP-2003;

JOURNAL

Location/Qualifiers

1. .2287

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7,67e-42 Length: 2287

Score: 675.00 Matches: 132

Percent Similarity: 100.00% Conservative: 0

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Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-4 (1-132) x AR403735 (1-2287)

Qy 1 ThrAlaAlaSerAspAsnProGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20

Db 63 ACGCCCGCTCCGATCACTTCCAGCTGCCAGGTGGGCGAGGATTCGCATTCGATC 122

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40

Db 123 GGGCAGCGCATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGTCAACCCCGTTCAT 182

Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60

Db 183 ATCGGGCTACCGCTTCTCGGCTTGGGTGTTCGACACACACGCGACGCGCACGA 242

Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

Db 243 GTCCAAACGGTGGTCCGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGCGGACGTG 302

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Db 303 ATCACCAGCGTCCGAGCGCTCCGATCACTCCGCCACCGGATCGCGAGCGCGCTTAAC 362

Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120

Db 363 GGGCATCATCCCGGTGACGTCTCGGTGACCTCGCAACCAAGTCGGGGCGGACGCGT 422

Qy 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132

Db 423 ACAGGAACGTGACATTGGCCGAGGACCCCGGCC 458

RESULT 10

AE006925

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

REFERENCE

1 (bases 1 to 14029)

Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,

Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,

Kolony,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,

Gill,J., Mikula,A. and Bishai,W.

TITLE

Whole genome comparison of Mycobacterium tuberculosis clinical and

laboratory strains

JOURNAL

Unpublished

2. (bases 1 to 14029)

Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,

Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,

Kolony,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,

Gill,J., Mikula,A. and Bishai,W.

Direct Submission

Submitted (25-APR-2001) The Institute for Genomic Research, 9712

JOURNAL

Medical Center Dr, Rockville, MD 20850, USA

Location/Qualifiers

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US-09-684-215B-4 (1-132) X AE006925 (1-14029)

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4248 GGGCAGCGATCGGATCGCGGCGCAGATCCGATCGGGTGGGGTCCACCCACCGTTTCAAT 4307

41 ileGlyProThraAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60

4308 ATCGGCGCTACCGCTTCCTCGGCTGGGTGTGTGCGACACACGCAACGCGCGCAGCA 4367

61 valGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80

4368 GTCCACGCGGTGTCGGGAGCGCTCCGGCGGCAAGTCTCGGATCTCCACCGCGCGCGT 4427

81 ileThraAlaValAspGlyAlaProIleAsnSerAlaThraAlaMetAlaAspAlaLeuAsn 100

4428 ATCACCGCGGTGACGCGCTCCGATCACTCGCCACCGCGATGCGGACGCGCTTAAC 4487

101 GlyHisHisProGlyAspValIleSerValThrTgGlnThrIleSerGlyGlyThrArg 120

4488 GGGCATCATCCCGGTGACGCTCATCTCGGTGACCTGGCAACCAAGTCGCGCGCGCGCGT 4547

121 ThrGlyAsnValThrLeuAlaGluGlyProAla 132

4548 ACAGGGAACGTGACATGGCCGAGGAGCCCGCGGCC 4583

RESULT 11

EX842572

ID BX842572 standard; circular genomic DNA; PRO; 341957 BP.

XX BX842572

AC BX842572; AL021427; AL021428; AL021927; AL021928; AL021929;

AC AL021930; AL123456; Z74410; Z80233; Z80775; Z86089; Z92669; Z92770; Z96071;

AC Z97050;

XX BX842572.1

XX 21-NOV-2003 (Rel. 77, Created)

DT 21-NOV-2003 (Rel. 77, Last updated, Version 1)

XX Mycobacterium tuberculosis H37Rv complete genome; segment 1/13

DE complete genome.

KW complete genome.

XX Mycobacterium tuberculosis H37Rv

OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;

OC Mycobacterium tuberculosis complex; Mycobacterium tuberculosis.

XX [1]

EN MEDLINE; 98295987.

FX PUBMED; 9634230.

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eigmeier K., Gas S., Barry III C.E., Tekala F., Badcock K.,

RA Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K.,

RA Felwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K.,

RA Krogan A., McLean J., Moule S., Murphy L., Oliver S., Osborne J.,

RA Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S.,

RA Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,

RT "Deciphering the biology of Mycobacterium tuberculosis from the complete

RT genome sequence";

RL Nature 393:537-544 (1998).

XX [2]

EN PUBMED; 12368430.

FX Camus J.C., Pryor M.J., Medigue C., Cole S.T.;

RA "Re-annotation of the genome sequence of Mycobacterium tuberculosis H37Rv";

RL Microbiology 148:2967-2973(2002).

XX [3]

EN 1-341957

RP Parkhill J.;

RT Submitted (11-JUN-1998) to the EMBL/GenBank/DBSJ databases.

RL Submitted on behalf of the Mycobacterium tuberculosis sequencing and

RL mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton,

RL Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut

RL Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail:

parkhill@sanger.ac.uk

Notes: Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/)

Key Location/Qualifiers

source 1. 341957

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/strain="H37Rv"

CDS 1. 1524

/evidence=EXPERIMENTAL

/note="RV0001, (MT0001, MT0029.01, P49993), len: 507 aa. dnaa, chromosomal replication initiator protein (see citations below); equivalent to other Mycobacterial CHROMOSOMAL REPLICATION INITIATOR PROTEINS e.g. P46388 [DNAA_MYCLE from Mycobacterium leprae (502 aa); Q9L7L7 [DNAA_MYCPA from Mycobacterium paratuberculosis (509 aa); P49990 [DNAA_MYCAV from Mycobacterium avium (508 aa); P49992 [DNAA_MYCSM from Mycobacterium smegmatis (504 aa); etc. Also highly similar to others except in N-terminus e.g. Q9ZH75 [DNAA_STRCH CHROMOSOMAL REPLICATION INITIATOR PROTEIN from Streptomyces chrysomallus (624 aa); Q9ZH76 [DNAA_STRRE from Streptomyces reticuli (643 aa); DNAA_ECOLI [P03004 | B3702 chromosomal replication initiator protein from Escherichia coli strain K12 (467 aa), FASTA scores: opt: 986, E(): 0, (43.2% identity in 389 aa overlap); etc. Contains PS00017 ATP/GTP-binding site motif A (P-loop) and PS01008 dnaa protein signature. BELONGS TO THE DNAA FAMILY. Note that the first base of this gene has been taken as base 1 of the Mycobacterium tuberculosis H37Rv genomic sequence."

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622.645

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1384.1440

/note="PS01008 Dnaa protein signature"

2052.3260

/evidence=EXPERIMENTAL

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misc_feature

misc_feature

CDS

in 337 aa overlap): P21174[DP3B_MICLU from Micrococcus
luteus (310 aa); P52023[DP3B_SINP7 from Synecococcus sp.
strain PCC 7942 (375 aa); etc. Overlaps and extends CDS in
neighbouring cosmid MTCV10H4.01."
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ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN
BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5'
EXONUCLEASE ACTIVITY. THE BETA CHAIN IS REQUIRED FOR
INITIATION OF REPLICATION ONCE IT IS CLAMPED ONTO DNA, IT
SLIDES FREELY (BIDIRECTIONAL AND ATP-INDEPENDENT) ALONG
DUPLICATED DNA [CATALYTIC ACTIVITY: N deoxynucleoside
triphosphate + N diphosphate + [DNA]N."
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/locus_tag="RV0002"
/product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA
NUCLEOTIDYLTRANSFERASE)"
/protein_id="CAA16239.1"
/translation="MDAATRVGLTDLTFLRLRESFADAVSWAKNLPARPAPVPLSGV
LITGSDNGITISGDFEVEAEAGAEIVPGSVLVSGRLISDITRALPNKPVDPVHVG
NRVALTCGNARSLPTMPVEDYPTPTPEETGLLPASLFAELASQVAIAAGRDITLPM
LTGIRVEILGETVLAATDRFLAVLEKWSASSPDIABAAVLVPKTLAEAKAGIGGS
DVRLSGTGPVGKGLGIGSGNKRSTRLDAEPFKFROLLPTEHTAVATMDKVAELI
EAKIYALVADRGAGVMEFADGSRVLSAGADDVGRAEEDLVVDYAGEPLTIAPNPTYL
TDGLSRLSERVSFGFTTACKFALLRPVSGDDRPVAGLNGNGFFPVESTDIVILMPVR
LPG"
3280..4437
/evidence=EXPERIMENTAL
/notes="RV0003, (MTCV10H4.01), len: 385 aa. recf, DNA
replication and repair protein (see citations below),
equivalent to others Mycobacterial DNA replication and
repair proteins e.g. NP 301131.1|NC 002677 from
Mycobacterium leprae (385 aa); Q9L755|REFC MYCPA from
Mycobacterium avium subsp. paratuberculosis (385 aa);
P50916|REFC MYCSM from Mycobacterium smegmatis (384 aa);
etc. Also highly similar to others e.g. P36176|REFC STRCO
DNA REPLICATION AND REPAIR PROTEIN from Streptomyces
coelicolor (373 aa); NP 440892.1|NC 000911 from
Synecocystis sp. strain PCC 6803 (384 aa);
NP 469152.1|NC 003212 from Listeria innocua (370 aa); etc.
Contains P800017 ATP/GTP-binding site motif A (P-loop),
P800617 Recf protein signature 1, and P800618 Recf protein
signature 2. BELONGS TO THE RECF FAMILY."
/transl_table=11
/function="THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM
AND RECOMBINATION; IT IS REQUIRED FOR DNA REPLICATION AND
NORMAL SOS INDUCIBILITY. RECF BINDS PREFERENTIALLY TO
SINGLE-STRANDED, LINEAR DNA. IT ALSO SEEMS TO BIND ATP."
/genes="recf"
/locus_tag="RV0003"
/product="DNA REPLICATION AND REPAIR PROTEIN RECF
(SINGLE-STRAND DNA BINDING PROTEIN)"
/protein_id="CAB02424.1"
/translations="MVRVHLGLRDFRSWACVLELHPGRTVFVPGNGYKTNLIEALWY
STLGLSHRVGADLPIRVGTDRAVIETIVNDGRCACVDELEATGRVKNKRLNRSVRS
TRDVGVGLRAVLPAESDLGLVGDPRDRRYLDDLAIVRPAIAAVERVRLQRTA
LLKSVGPARVGRGVPTDLEWDSLAESHGLVLAARDLVNQLAPVKYQQLAPE
SRASGIGTASMDVTPSGQSDIDRQLAARLLAALAAARDLAERGLVGLVPHRDDLI
LRIGDPAKGFASGSEANSLAVALAAVOLLRVGDEPVLILLDDVFAELDDVMRRRLA
TAASAEQVLVTAALVEDIPAGWDARVHIDVRADDTGSMGVLP"
3367..3390
/note="P800017 ATP/GTP-binding site motif A"
/note="P800617 Recf protein signature 1"
/note="P800618 Recf protein signature 2"
/note="P800618 Recf protein signature 2"
4434..4997
/evidence=EXPERIMENTAL
/note="RV0004, (MTCV10H4.02), len: 187 aa. Conserved
hypothetical protein (see Salazar et al., 1996), highly
similar, but longer 21 aa in N-terminus, to
AAE33696.1|AF222789 unknown protein from Mycobacterium

FT avium subsp. paratuberculosis (166 aa); and highly similar
FT to NP_301132.1|NC_002677 conserved hypothetical protein
FT from Mycobacterium leprae (189 aa); S70990 hypothetical
FT protein from Mycobacterium smegmatis (194 aa). Also highly
FT similar, except in N-terminal part, to

Alignment Scores:

Pred. No.: 1-126-39 Length: 341957
Score: 675.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-4 (1-132) x BX842572 (1-341957)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 151817 ACGGCCGCTCGGATTAATTCAGCTGCCAGGGTGGCAGGATTCCGCATCCCGATC 151876
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
Db 151877 GGGCAGCGCATCGCATCGGGCCAGATCCGATCGGCTGGGGGTCAACCCACCGTTTCAT 151936
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValAlaArg 60
Db 151937 ATCGGCGCTTACCGCTTCTCGGCTTGGGTGTGTCGACAAACAGCGCAACGGCGCACA 151996
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 151997 GTCCACCGCTGGTGGGAGCGCTCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG 152056
QY 81 IleThrAlaValAlaAspGlyAlaProIleLeuSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 152057 ATCCCGCGGTGACGGCGCTCCGATCAACTCGGCACCGGATGGCGGACGGCTTAAAC 152116
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 152117 GGGCATCATCCCGGTGACGTCACTCGGTACCTGGCAACCAAGTCCGGGGCGGCGCGGT 152176
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 152177 ACAGGGAACGTGACATTGGCCGAGGAGACCCCGCGGC 152212

RESULT 12

BX248334

LOCUS

DEFINITION

1/14

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

PNAS 10.1073/pnas.1130426100 (Microbiology)

2 (bases 1 to 343050)

Garnier,T.

Direct Submission

Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire

Bacterienne Institut Pasteur 28,rue du Dr Roux 75724 PARIS cedex

15, France, e-mail:tgarnier@pasteur.fr Submitted on behalf of the

Mycobacterium bovis sequencing teams, TB Research Group, Veterinary

Research Group, Veterinary

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P21174|D3B3_MICU from Micrococcus luteus (310 aa);
P52023|D3B3_SYN7 from Synecoccus sp. strain PC7 7942
(375 aa); etc. Overlaps and extends CDS in neighbouring
cosmid MTCY10H4.01."
/codon_start=1
/evidence=experimental
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product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA NUCLEOTIDYLTRANSFERASE)"
protein_id="CAD92864.1"
db_xref="GI:31618764"
translation="MDAATRVGLDTFRLRESFADAVSWAKNLPARPAPVLSG

EGNRVALTCGNARFSLPTMPVEDYPTLPTLPEETGLLPABLFAEASISQVAIAAGRDDU
LPMLTGIRVEILGETVLAATDRFLAVRELKWSASSPDIEAAVLVPAKTLAEAAKAG
IGGSDVRLSLGTGPGVGKDLLGISNGKRSSTRLLDAEFPKFRQLPTEHTAVATMD

VAEIIIAIKALIVADVGRQAQVMEFADGSAVDVGRABEDLVVDVAGSEPLTIV
 FNPTYLTDGLSSLSRSEVSFVGFETTAGKALLRPVSGDDRPVAGLNGNGPPFPAVSTDYV
 YLAMPVRLPC"

3280. 4437
 /gene="recF"
 /locus_tag="Mb00003"
 3280. 4437
 /gene="recF"
 /locus_tag="Mb00003"
 /note="Mb0003, recF, len: 385 aa. Equivalent to RV0003,
 len: 385 aa, from Mycobacterium tuberculosis strain H37Rv,
 (99.5% identity in 385 aa overlap). recF, DNA replication
 and repair protein (see citations below), equivalent to
 others Mycobacterial DNA replication and repair proteins
 e.g. NP_301131.1|NC_002677 from Mycobacterium leprae (385
 aa); Q57L15|REFC MYCPA from Mycobacterium avium subsp.
 paratuberculosis (385 aa); P50916|REFC MYCSM from
 Mycobacterium smegmatis (384 aa); etc. Also highly similar
 to others e.g. P16176|REFC SPTFCO DNA REPLICATION AND
 REPAIR PROTEIN from Streptomyces coelicolor (373 aa);
 NP_440892.1|NC_000911 from Synecocystis sp. strain PCC
 6803 (384 aa); NP_469352.1|NC_003212 from Listeria innocua
 (370 aa); etc. Contains P50017 ATG/GRP-binding site motif

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RecF protein signature 2. BELONGS TO THE REC F FAMILY. W
/codon_start=1
/evidence=experimental
/transl_table=11
/product=DNA REPLICATION AND REPAIR PROTEIN REC F

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>protein_id="CA9292865.1"
/db_xref="GI:31616765"
>translation="MYVRLHGTDRFSWACVLDLHPGRTVFGNGVKNLTLEALW
YSTTLGSHRYVADLPILRVLTGDAVSTITVNDGRCVADLIEATGRVYKNLRNRS
RSTEDVGVTVAVLPAEDGLVGRGPDARVYLDLIAIVRPAITAAVRVAVRVCR
TALLKVPGNRGVGRGVDTLKVNDSPRLAEGHLEADLVNQLAIPVKAYQVL
LAPSRSGYIRASHEDTQPSQSTDTQLLAAPLAAALAAARDPAELRGVCLNGPHE
RDDLILRGQGPAGFASGAEWLSVALKLAAYLLRVLDGGEPTVLDDYPAELDVN
RRRLAAASAEQVLVVALESDIIPAGMDARVHLDVRADDTGMSVLP"

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gene

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/locus_tag="Mb0004"
4434..4997
/locus_tag="Mb0004"
/note="Mb0004, -, len: 187 aa. Equivalent to Rv0004, len:
187 aa, from Mycobacterium tuberculosis strain H37Rv,"

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protein (see citation below), highly similar to streptococcal protein (in N-terminus, to AAF33696.1) AF222789 unknown protein from *Mycobacterium avium* subsp. *paratuberculosis* (166 aa) and highly similar to NP_301132.1|NC_002677 (166 aa) and conserved hypothetical protein from *Mycobacterium leprae* (189 aa); S70390 hypothetical protein from *Mycobacterium smegmatis* (194 aa). Also similar to in C-terminus to C-terminal part of P35925|YREG SPRCO HYPOTHEICAL 19.8 KDa PROTEIN (IN RSCF-GYR8 INTERGENIC REGION) from *Streptomyces coelicolor* (190 aa), FASTA scores: opt: 44%, E(): 3.9e-18 (40.7% identity in 189 aa overlap).

/codon_start=1
/transl_table=11
/product="CONSERVED HYPOTHETICAL PROTEIN"
/protein_id="CAD92866.1"
/db_xref="GI:31616766"
/translation="MTGSVPRPQNGERLWKSPGLVRLTIDEARAAARQDAG
RGRVASVAGRGVAGRRSGWGPEDRDQPLGKAARELAKKMGVSRVAVGWLQW
SAVGHQIAEHARTALNDGVLVIAESTAWATQIRIMQAQLAKIAAAVGNVDVRS
KITGPAAPSWRKGPRIHAGRPRTYG"
gene 5123..7267
/gene="gyrB"
/locus_tag="Mb0005"
CDS 5123..7267
/gene="gyrB"
/locus_tag="Mb0005"
/EC_number="5.99.1.3"
/note="Mb0005, gyrB, len: 714 aa. Equivalent to Rv0005,
len: 714 aa, from Mycobacterium tuberculosis strain H37RV,
(99.9% identity in 714 aa overlap). gyrB, DNA gyrase
subunit B (EC 5.99.1.3) (see citations below), equivalent,
except in N-terminus, to other Mycobacterial DNA GYRASES
SUBUNIT B e.g. T10005 from Mycobacterium leprae (697 aa);
Q9L7L3 (GYR MYCPA from Mycobacterium avium subsp.
paratuberculosis (677 aa) (has its N-terminus shorter);
P48355 (GYR MYCSM from Mycobacterium smegmatis (675 aa);
etc. Also highly similar to others e.g. T10969 from
Streptomyces coelicolor (686 aa); P50075 (GYBS_STRSH from

Alignment Scores:
Pred. No.: 1.12e-39 Length: 343050
Score: 675.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-684-215B-4 (1-132) x BX248334 (1-343050)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 152008 ACGGCCGCGTCCGATTAACCTCCAGCTGTCACAGGCTGGGCGAGGATTCGCCATTCCGATC 152067
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 152068 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCAACCCCGCTTAC 152127
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValAlaArg 60
Db 152128 ATCGGCCCTACCCCTTCCTCGCTGGGTGGTGTGTCACACACGCAACCGCGCAGCA 152187
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 152188 GTCCACGCGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGCATCTCCACCGCGCGACGTG 152247
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 152248 ATCACCAGCGTGCAGCGCGCTCCGATCACTCGGCCACCGCATCGCGCGCTTAAC 152307
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 152308 GGGCATCATCCGCTGACGTCATCTCGGTGACCTGCGCAACCAAGTCGGCGCGCACGCT 152367
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 152368 ACAGGGAACGTGACATTGGCGGAGGGACCCCGGCC 152403

RESULT 13
LOCUS AR169152
DEFINITION Sequence 4 from patent US 6290969.
ACCESSION AR169152
VERSION AR169152.1 GI:17906927
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R.,
Vedvick,T.S. and Twardzik,D.R.
TITLE Compounds and methods for immunotherapy and diagnosis of
tuberculosis
JOURNAL Patent: US 6290969-A 4 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..447
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.59e-42 Length: 447
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-4 (1-132) x AR169152 (1-447)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCCGCGTCCGATTAACCTCCAGCTGTCACAGGCTGGGCGAGGATTCGCCATTCCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGCGATGCGATCGCGGCCAGATCCGATCGGGTGGGGGTCAACCCCGCTTAC 130
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValAlaArg 60
Db 131 ATCGGCCCTACCCCTTCCTCGCTGGGTGGTGTGTCACACCAACCGCAACCGCGCACGA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACGCGTGGTGGGAGCGCTCCGCGCGCAAGTCTCGGCATCTCCACCGCGCGGTG 250
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCACCAGCGTGCAGCGCGCTCCGATCACTCGGCCACCGCATCGCGCGCTTAAC 310
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 311 GGGCATCATCCGCTGACGTCATCTCGGTGAACTGGCAACCAAGTCGGCGCGCACGCT 370
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 371 ACAGGGAACGTGACATTGGCGGAGGGACCCCGGCC 406

RESULT 14
LOCUS AR182442
DEFINITION Sequence 4 from patent US 633852.
ACCESSION AR182442
VERSION AR182442.1 GI:20225649
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R.,
Vedvick,T.S. and Twardzik,D.R.
TITLE Compounds and methods for diagnosis of tuberculosis
JOURNAL Patent: US 633852-A 4 15-JAN-2002;
FEATURES Location/Qualifiers
source 1..447
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores: 3.59e-42 Length: 447
 Pred. No.: 670.00 Matches: 131
 Score: 99.24% Conservative: 0
 Percent Similarity: 99.24% Mismatches: 1
 Best Local Similarity: 99.24% Indels: 0
 Query Match: 99.26% Gaps: 0
 DB: 6

US-09-684-215B-4 (1-132) x AR182442 (1-447)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 11 ACGGCGCGTCCGATTAACCTCCAGCTGTCAGGCTGGGAGGATCCGATTCGATC 70
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 DB 71 GGGCAGCGGATCGGATCGGCGGCGGATCCGATCGGCTGGGAGGATCCGATTCGATC 130
 QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
 DB 131 ATCGGCGCTACCGCTTCCTCGGCTTGGTGTTCGACAAACGCGGACGCGACGA 190
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 191 GTCCAAACGCGTGGTGGGAGCGCTCCGCGGCGGAGTCTCGGATCTCCACCGGACGTG 250
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 DB 251 ATCACCGCGGTGCGAGCGGCTCCGATCACTCGGCACCGGATGCGGACGCGCTTAAC 310
 QY 101 GlyHisHisProGlyAspValIleSerValThrTyrGlnThrIlysserGlyGlyThrArg 120
 DB 311 GGGCATCATCCGCTGACGTCATCTCGGTGAACCTGCGCAACCAAGTGGGCGGACGCGT 370
 QY 121 ThrGlyAsnValThrLeuAlaGlyGlyProProAla 132
 DB 371 ACAGGGAACGTGACATTGGCGGAGGACCCCGGCC 406

RESULT 16
 AR233097
 LOCUS
 DEFINITION Sequence 4 from patent US 6458366.
 ACCESSION AR233097
 VERSION AR233097.1 GI:27275533
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 447)
 AUTHORS Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.
 TITLE Compounds and methods for diagnosis of tuberculosis
 JOURNAL Patent: US 6458366-A 4 01-OCT-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores: 3.59e-42 Length: 447
 Pred. No.: 670.00 Matches: 131
 Score: 99.24% Conservative: 0
 Percent Similarity: 99.24% Mismatches: 1
 Best Local Similarity: 99.24% Indels: 0
 Query Match: 99.26% Gaps: 0
 DB: 6

US-09-684-215B-4 (1-132) x AR233097 (1-447)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 11 ACGGCGCGTCCGATTAACCTCCAGCTGTCAGGCTGGGAGGATTCGATTCGATC 70
 QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 DB 71 GGGCAGCGGATCGGATCGGCGGCGGATCCGATCGGCTGGGAGGATCCGATTCGATC 130
 QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
 DB 131 ATCGGCGCTACCGCTTCCTCGGCTTGGTGTTCGACAAACGCGGACGCGACGA 190
 QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 DB 191 GTCCAAACGCGTGGTGGGAGCGCTCCGCGGCGGAGTCTCGGATCTCCACCGGACGTG 250
 QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

RESULT 15
 AR194825
 LOCUS
 DEFINITION Sequence 4 from patent US 6350456.
 ACCESSION AR194825
 VERSION AR194825.1 GI:20244262
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 447)
 AUTHORS Read, S.G., Skeiky, Y.A.W. and Dillon, D.C.
 TITLE Compositions and methods for the prevention and treatment of M.
 tuberculosis infection
 JOURNAL Patent: US 6350456-A 4 26-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Alignment Scores: 3.59e-42 Length: 447
 Pred. No.: 670.00 Matches: 131
 Score: 99.24% Conservative: 0
 Percent Similarity: 99.24% Mismatches: 1
 Best Local Similarity: 99.24% Indels: 0
 Query Match: 99.26% Gaps: 0
 DB: 6

US-09-684-215B-4 (1-132) x AR194825 (1-447)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 11 ACGGCGCGTCCGATTAACCTCCAGCTGTCAGGCTGGGAGGATTCGATTCGATC 70

Db 251 ATACCGCGTGGACGGCTCCGATCACTCGCCACCGGATGGCGACGGCTTAAC 310
 Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 Db 311 GGGCATCATCCGCTGAGCTCATCTCGGTGAACCTGGCAACCAAGTCGGCGGCACGCGT 370
 Qy 121 ThrGlyAsnValThrLeuAlaGluGlyProAla 132
 Db 371 ACAGGGAACGTGACATTGGCCGAGGACCCCGGCC 406

RESULT 17
 AR353302
 LOCUS AR353302 447 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 4 from patent US 6592877.
 ACCESSION AR353302
 VERSION AR353302.1 GI:33759108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 447)
 AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
 Vedwick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.
 TITLE Compounds and methods for immunotherapy and diagnosis of
 tuberculosis
 JOURNAL Patent: US 6592877-A 4 15-JUL-2003;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores: 3.59e-42 Length: 447
 Pred. No.: 670.00 Matches: 131
 Score: 99.24% Conservative: 0
 Percent Similarity: 99.24% Mismatches: 1
 Best Local Similarity: 99.24% Indels: 0
 Query Match: 99.26% Gaps: 0
 DB: 6

US-09-684-215B-4 (1-132) x AR353302 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 Db 11 ACGGCGCGTCCGATAAATCCAGCTGTCCAGGGTGGCGAGGGATTCGCCATTCGGATC 70
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 Db 71 GGCAGCGATGGCGATCCGGGCCAGATCCGATCGGTGGGGGTCAACCCACCGTTTCAT 130
 Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
 Db 131 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTGCAACAACGCGCAACGCGCACGA 190
 Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 191 GTCACCGCGTGGAGCGCTCCGGCGGAGCTCCGGCGGAGTCTCGGCATCTCCACCGCGCTTAC 250
 Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 Db 251 ATCACCAGCGTCCGACGGCTCCGATCACTCGGCCACCGCGATGGCGGACGGCTTAAC 310
 Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 Db 311 GGGCATCATCCCGTGAACGTCATCTCGTGAATCTGGCAACCAAGTCGGCGGCACGCGT 370

RESULT 18
 AX429596
 LOCUS AX429596 447 bp DNA linear PAT 12-DEC-2003
 DEFINITION Sequence 4 from Patent EP1203817.
 ACCESSION AX429596
 VERSION AX429596.1 GI:21540845
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,
 Vedwick, T.S. and Twardzik, D.R.
 TITLE Compounds and methods for immunotherapy and diagnosis of
 tuberculosis
 JOURNAL Patent: EP 1203817-A 4 08-MAY-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Alignment Scores: 3.59e-42 Length: 447
 Pred. No.: 670.00 Matches: 131
 Score: 99.24% Conservative: 0
 Percent Similarity: 99.24% Mismatches: 1
 Best Local Similarity: 99.24% Indels: 0
 Query Match: 99.26% Gaps: 0
 DB: 6

US-09-684-215B-4 (1-132) x AX429596 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 Db 11 ACGGCGCGTCCGATAAATCCAGCTGTCCAGGGTGGCGAGGGATTCGCCATTCGGATC 70
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 Db 71 GGCAGCGATGGCGATCCGGGCCAGATCCGATCGGTGGGGGTCAACCCACCGTTTCAT 130
 Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
 Db 131 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTGCAACAACGCGCAACGCGCACGA 190
 Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 191 GTCACCGCGTGGAGCGCTCCGGCGGAGCTCCGGCGGAGTCTCGGCATCTCCACCGCGCTTAC 250
 Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 Db 251 ATCACCAGCGTCCGACGGCTCCGATCACTCGGCCACCGCGATGGCGGACGGCTTAAC 310
 Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 Db 311 GGGCATCATCCCGTGAACGTCATCTCGTGAATCTGGCAACCAAGTCGGCGGCACGCGT 370

RESULT 19
 AX832581
 LOCUS AX832581 447 bp DNA linear PAT 12-DEC-2003
 DEFINITION Sequence 4 from Patent EP1347055.
 ACCESSION AX832581
 VERSION AX832581.1 GI:39840631
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
 Vedwick, T.S., Twardzik, D.R. and Dillon, D.C.

LOCUS AX429596 447 bp DNA linear PAT 21-JUN-2002
 DEFINITION Sequence 4 from Patent EP1203817.
 ACCESSION AX429596
 VERSION AX429596.1 GI:21540845
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,
 Vedwick, T.S. and Twardzik, D.R.
 TITLE Compounds and methods for immunotherapy and diagnosis of
 tuberculosis
 JOURNAL Patent: EP 1203817-A 4 08-MAY-2002;
 FEATURES Location/Qualifiers
 source 1..447
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
 Alignment Scores: 3.59e-42 Length: 447
 Pred. No.: 670.00 Matches: 131
 Score: 99.24% Conservative: 0
 Percent Similarity: 99.24% Mismatches: 1
 Best Local Similarity: 99.24% Indels: 0
 Query Match: 99.26% Gaps: 0
 DB: 6

US-09-684-215B-4 (1-132) x AX429596 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 Db 11 ACGGCGCGTCCGATAAATCCAGCTGTCCAGGGTGGCGAGGGATTCGCCATTCGGATC 70
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
 Db 71 GGCAGCGATGGCGATCCGGGCCAGATCCGATCGGTGGGGGTCAACCCACCGTTTCAT 130
 Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyAsnGlyAlaArg 60
 Db 131 ATCGGGCTTACCGCTTCTCGGCTTGGGTGTGTGCAACAACGCGCAACGCGCACGA 190
 Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
 Db 191 GTCACCGCGTGGAGCGCTCCGGCGGAGCTCCGGCGGAGTCTCGGCATCTCCACCGCGCTTAC 250
 Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
 Db 251 ATCACCAGCGTCCGACGGCTCCGATCACTCGGCCACCGCGATGGCGGACGGCTTAAC 310
 Qy 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
 Db 311 GGGCATCATCCCGTGAACGTCATCTCGTGAATCTGGCAACCAAGTCGGCGGCACGCGT 370

RESULT 19
 AX832581
 LOCUS AX832581 447 bp DNA linear PAT 12-DEC-2003
 DEFINITION Sequence 4 from Patent EP1347055.
 ACCESSION AX832581
 VERSION AX832581.1 GI:39840631
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
 Vedwick, T.S., Twardzik, D.R. and Dillon, D.C.

TITLE Compounds for immunotherapy and diagnosis of tuberculosis
JOURNAL Patent: EP 1347055-A 4 24-SEP-2003;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..447
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 3.59e-42 Length: 447
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservativeness: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-4 (1-132) x AX832581 (1-447)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
Db 11 ACGGCGCGGTCCGATAACTTCCAGCTGTCAGAGGTGGCGAGGATTCGCCATTCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGGCGATGGCGATCGCGGCGAGATCCGATCGGTGGGGGTCAACCCACCTTCAT 130
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAsnGlyValAlaArg 60
Db 131 ATCGGCGCTACCGCTTCTCGGCTGGGTGTGTGTCGACAAACGCGCAACGGCGCACGA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCAAACGGGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGATCTCCACCGGCGACGTG 250
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCAGCGCGTGCAGCGCGCTCCGATCACTCGGCCACCGCGATGGCGAGCGCTTAAC 310
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 311 GGGCATCATCCCGGTGACGTCTCTCGGTGAACCTGGCAACCAACGTCGGGCGGCGACGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 371 ACAGGAGACGTGACATTTGGCCGAGGACCCCGGCC 406

RESULT 20
BD006325
LOCUS 447 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for diagnosis of Tuberculosis.
ACCESSION BD006325
VERSION BD006325.1 GI:18634596
KEYWORDS JP 2001500383-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R.,
Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
TITLE Compounds and methods for diagnosis of Tuberculosis
JOURNAL Patent: JP 2001500383-A 4 16-JAN-2001;
CORIXA CORP
COMMENT OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PF 07-OCT-1997 JP 1998518432
PR 11-OCT-1996 US 08/729622,13-MAR-1997 US 08/818111 PI
STEVEN G REED,VASIR A W SKEIKY,DAVIN C DILLON, PI ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK, PI
MICHAEL J LODES

PC C12N15/31,C07K14/35,C07K16/12,C12Q1/68,C12N15/62,G01N33/53 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..447
/organism="unidentified".

FEATURES

source 1..447
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 3.59e-42 Length: 447
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservativeness: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-4 (1-132) x BD006325 (1-447)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
Db 11 ACGGCGCGGTCCGATAACTTCCAGCTGTCAGAGGTGGCGAGGATTCGCCATTCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGGCGATGGCGATCGCGGCGAGATCCGATCGGTGGGGGTCAACCCACCTTCAT 130
QY 41 IleGlyProThrAlaPheLeuGlyValValAspAsnGlyValAsnGlyValAlaArg 60
Db 131 ATCGGCGCTACCGCTTCTCGGCTGGGTGTGTGTCGACAAACGCGCAACGGCGCACGA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCAAACGGGTGGTGGGAGCGCTCCGCGGCAAGTCTCGGATCTCCACCGGCGACGTG 250
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCAGCGCGTGCAGCGCGCTCCGATCACTCGGCCACCGCGATGGCGAGCGCTTAAC 310
QY 101 GlyHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 311 GGGCATCATCCCGGTGACGTCTCTCGGTGAACCTGGCAACCAACGTCGGGCGGCGACGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 371 ACAGGAGACGTGACATTTGGCCGAGGACCCCGGCC 406

RESULT 21
BD006445
LOCUS 447 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for immunotherapy and diagnosis of
Tuberculosis.
ACCESSION BD006445
VERSION BD006445.1 GI:18634816
KEYWORDS JP 2001501832-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R.,
Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
TITLE Compounds and methods for immunotherapy and diagnosis of
JOURNAL Patent: JP 2001501832-A 4 13-FEB-2001;
CORIXA CORP
COMMENT OS Unidentified
PN JP 2001501832-A/4
PD 13-FEB-2001
PF 07-OCT-1997 JP 1998518456
PR 11-OCT-1996 US 08/730510,13-MAR-1997 US 08/818112 PI

STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31, C07K14/35, A61K39/04, A61K48/00, A61K49/00, C12N15/62,
PC C07K19/00,
PC G01N33/50, G01N33/60, G01N33/569, C12N1/19, C12N1/20, C12N1/21, PC
C12N5/10/
PC (C12N1/21, C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..447 /organism="Unidentified".
FT Location/Qualifiers
1..447 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 3.59e-42 Length: 447
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-4 (1-132) x BD066445 (1-447)

QY 1 ThrAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 11 ACGGCCGGTCCGATTAACCTCCAGCTGTCGAGGGTGGCAGGGATTCGCCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGCGATGGCGATCGCGGGCCAGATCGATCGGTGGGGGTCCACCCCGTTTAT 130
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArg 60
Db 131 ATCGGGCTACCGCTTCTCGGCTTGGGTGTGTCGACAAACGCGACGGCGCACCA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACCGGTGGTGGGAGCGCTCCGGGGCAAGTCTCGCATCTCCACCGCGACGTG 250
QY 81 IleThrAlaValAspGlyAlaProAlaProAlaSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCCCGCGTCCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGACGGCTTAAC 310
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 311 GGGCATCATCCCGTGACGTCTCTCGGTGAACCTGGCAACCAAGTCCGGCGGCGACGGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 371 ACAGGGAACGTGACATTGGCGAGGGACCCCGGCC 406

RESULT 22
BD069285
LOCUS 447 bp DNA linear PAT 27-AUG-2002
DEFINITION Compounds and methods for immunotherapy and diagnosis of
tuberculosis.

ACCESSION
VERSION BD069285.1 GI:22614888
KEYWORDS JP 2001517069-A/4.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
Vedvick, T.H. and Twardzik, D.R.

TITLE
JOURNAL
COMMENT

Compounds and methods for immunotherapy and diagnosis of
Patent: JP 2001517069-A 4 02-OCT-2001;
COREIXA CORP
OS Unidentified
FN JP 2001517069-A/4
PD 02-OCT-2001
PF 30-AUG-1996 JP 1997511464
PR 01-SEP-1995 US 08/523436, 22-SEP-1995 US 08/533634 PR
22-MAR-1996 US 08/620874, 05-JUN-1996 US 08/659683 PR
12-JUL-1996 US 08/680574
PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS
PI NETO,
PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC
C12N15/31, C07K14/35, A61K38/16, C12N15/62, G01N33/569, C12Q1/68, PC
C12N5/10,
PC C12N1/21//A61K39/04, (C12N1/21, C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
CC Compounds and methods for immunotherapy and diagnosis of CC
tuberculosis
FH Key Location/Qualifiers
FT source 1..447 /organism="Unidentified".
FT Location/Qualifiers
1..447 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 3.59e-42 Length: 447
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-4 (1-132) x BD069285 (1-447)

QY 1 ThrAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 11 ACGGCCGGTCCGATTAACCTCCAGCTGTCGAGGGTGGCAGGGATTCGCCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGCGATGGCGATCGCGGGCCAGATCGATCGGTGGGGGTCCACCCCGTTTAT 130
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArg 60
Db 131 ATCGGGCTACCGCTTCTCGGCTTGGGTGTGTCGACAAACGCGACGGCGCACCA 190
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACCGGTGGTGGGAGCGCTCCGGGGCAAGTCTCGCATCTCCACCGCGACGTG 250
QY 81 IleThrAlaValAspGlyAlaProAlaProAlaSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATCCCGCGTCCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGACGGCTTAAC 310
QY 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIleSerGlyGlyThrArg 120
Db 311 GGGCATCATCCCGTGACGTCTCTCGGTGAACCTGGCAACCAAGTCCGGCGGCGACGGGT 370
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 371 ACAGGGAACGTGACATTGGCGAGGGACCCCGGCC 406

RESULT 23
BD05817
LOCUS 447 bp DNA linear PAT 17-JUL-2003
DEFINITION Compounds and methods for diagnosis of tuberculosis.
ACCESSION BD05817

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VERSION      BD205817.1  GI:33015587
KEYWORDS     JP 2002530050-A/4.
SOURCE       Mycobacterium tuberculosis
ORGANISM     Mycobacterium tuberculosis
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
              tuberculosis complex.
REFERENCE    1 (bases 1 to 447)
AUTHORS     Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R.,
              Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
TITLE       Compounds and methods for diagnosis of tuberculosis
JOURNAL     Patent: JP 2002530050-A 4 17-SEP-2002;
              CORIXA CORP
COMMENT     OS Mycobacterium tuberculosis
              PN JP 2002530050-A/4
              PD 17-SEP-2002
              PF 17-FEB-1999 JP 2000532132
              PR 18-FEB-1998 US 09/024753, 05-MAY-1998 US 09/072596 PI
              STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI
              NETO,
              PI RAYMOND HOUGHTON, THOMAS S VEDVICK, DANIEL R TWARDZIK, MICHAEL J
              PI LODES,
              PI RONALD C HENDRICKSON
              PC C12N15/09, C07H21/02, C07H21/04, C07K7/00, C07K14/35, C07K16/12, PC
              C07K17/00,
              PC C07K19/00, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/04, C12Q1/
              PC 68,
              PC GOIN33/569, GOIN33/68//A61K38/00, A61K39/04, A61K39/395, A61K39/
              PC 395, A61P31/06,
              PC (C12N1/21, C12R1:19), C12N15/00, C12N5/00, A61K37/02 CC
              Compounds and methods for diagnosis of tuberculosis. FH Key
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              FT /organism="Mycobacterium tuberculosis".

FEATURES     source
              Location/Qualifiers
              1..447
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              /mol_type="genomic DNA"
              /db_xref="taxon:1773"

ORIGIN
Alignment Scores:
Pred. No.: 3,598-42 Length: 447
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-4 (1-132) x BD205817 (1-447)
Qy 1 ThrAlaAlaSerAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGCCCGCTCCGATTAACCTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGGATC 70
Qy 21 GlyAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 71 GGGCAGCGATGGCGATCGGGGCGAGATCCGATCCGATCGGGTGGGGGTCAACCACCGTTCAT 130
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAenglyValaArg 60
Db 131 ATCGGGCTACCGCTTCCGGCTTGGGTGTGTCGACAAACGCGACGCGCACGA 190
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 191 GTCCACCGCTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 250
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 251 ATACCGCGGTGCGAGCGCTCCGATCACTCGGCCACCGGATGGCGGCGCTTAAC 310
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyGlyThrArg 120

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311 GGGCATCATCCCGTGGTACGTGATCTCGTGAACCTGGAACCAACCAAGTCGGGCGGACGCGT 370
Qy 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 371 ACAGGGAACGTGACATTCGGCCGAGGAGACCCCGGCC 406

RESULT 24
AR169165 LOCUS 1872 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6290969.
ACCESSION AR169165
VERSION AR169165.1 GI:17906947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1872)
AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
              Vedvick, T.S., and Twardzik, D.R.
TITLE Compounds and methods for immunotherapy and diagnosis of
              tuberculosis
JOURNAL Patent: US 6290969-A 17 18-SEP-2001;
FEATURES Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1,498-41 Length: 1872
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-4 (1-132) x AR169165 (1-1872)
Qy 1 ThrAlaAlaSerAspAsnPhelGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACGCCCGCTCCGATTAACCTCCAGCTGTCCAGGGTGGGAGGATTCGCCATTCGGATC 817
Qy 21 GlyAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGCGATGGCGATCGGGGCGCAATCCGATCCGATCGGGTGGGGGTCAACCACCGTTCAT 877
Qy 41 IleGlyProThrAlaPheLeuGlyValValAspAsnAenglyValaArg 60
Db 878 ATCGGGCTACCGCTTCCGGCTTGGGTGTGTCGACAAACGCGACGCGCACGA 937
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 938 GTCCACCGCTGGTGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 997
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATACCGCGGTGCGAGCGCTCCGATCACTCGGCCACCGGATGGCGGCGCTTAAC 1057
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrIlysserGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGTGGTACGTGATCTCGTGAACCTGGAACCAACCAAGTCGGGCGGACGCGT 1117
Qy 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
Db 1118 ACAGGGAACGTGACATTCGGCCGAGGAGACCCCGGCC 1153

RESULT 25
AR182455 LOCUS 1872 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 17 from patent US 6338852.
ACCESSION AR182455
VERSION AR182455.1 GI:20225662
KEYWORDS

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[illegible]

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlySerProThrValHis 40
DB 818 GGGCAGCGATGGGATCGCGGGCCAAATCCGATCGGTGGGGGTACCCACCGTTTCA 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValHis 60
DB 878 ATCCGGGCTTACCGCTTCCCTCGGCTGGGTGGTGTGTCGACAAACACGCGACGCA 937
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 938 GTCCACGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 998 ATCACCAGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 1057
QY 101 GlyHisProGlyAspValIleSerValThrTriPnThrLysSerGlyGlyThrArg 120
DB 1058 GGGCATCATCCCGTGGTACGTCATCTCGTGAACCTGGCAACCAAGTCGGGCGGACGCGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
DB 1118 ACAGGGAACGTGACATTTGGCGAGGACCCCGGCC 1153
RESULT 28
AR353315
LOCUS AR353315 1872 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 17 from patent US 6592877.
ACCESSION AR353315
VERSION AR353315.1 GI:33759121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1872)
AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.
TITLE Compounds and methods for immunotherapy and diagnosis of
tuberculosis
JOURNAL Patent: US 6592877-A 17 JUL-2003;
FEATURES
source Location/Qualifiers
1..1872
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1,498-41 Length: 1872
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-4 (1-132) x AR353315 (1-1872)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
DB 758 ACGGCGCGTCCGATAAATCCAGCTGTCACGAGGTGGGCGAGGATTCGCCATTCGATC 817
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 818 GGGCAGCGATGGGATCGCGGGCCAAATCCGATCGGTGGGGGTACCCACCGTTTCA 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValHis 60
DB 878 ATCCAGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 938 GTCCACGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

DB 998 ATCACCAGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 1057
QY 101 GlyHisProGlyAspValIleSerValThrTriPnThrLysSerGlyGlyThrArg 120
DB 1058 GGGCATCATCCCGTGGTACGTCATCTCGTGAACCTGGCAACCAAGTCGGGCGGACGCGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
DB 1118 ACAGGGAACGTGACATTTGGCGAGGACCCCGGCC 1153
RESULT 29
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LOCUS AR429609 1872 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 17 from Patent EP1203817.
ACCESSION AR429609
VERSION AR429609.1 GI:21540858
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,
Vedvick, T.S. and Twardzik, D.R.
TITLE Compounds and methods for immunotherapy and diagnosis of
tuberculosis
JOURNAL Patent: EP 1203817-A 17 08-MAY-2002;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 1,498-41 Length: 1872
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 0
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0
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QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
DB 818 GGGCAGCGATGGGATCGCGGGCCAAATCCGATCGGTGGGGGTACCCACCGTTTCA 877
QY 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnGlyValHis 60
DB 878 ATCCAGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
DB 938 GTCCACGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 997
QY 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
DB 998 ATCACCAGCGTGTGCGAAGCGCTCGCGGCGCAAGTCTCGGCATCTCCACCGCGACGTG 1057
QY 101 GlyHisProGlyAspValIleSerValThrTriPnThrLysSerGlyGlyThrArg 120
DB 1058 GGGCATCATCCCGTGGTACGTCATCTCGTGAACCTGGCAACCAAGTCGGGCGGACGCGT 1117
QY 121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
DB 1118 ACAGGGAACGTGACATTTGGCGAGGACCCCGGCC 1153

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RESULT 30
AX832594
LOCUS AX832594 1872 bp DNA linear PAT 12-DEC-2003
DEFINITION Sequence 17 from Patent EP1347055.
ACCESSION AX832594
VERSION AX832594.1 GI:39840644
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 Reed, S.G., Skeiky, Y.A., Campos-Neto, A., Houghton, R.L.,
AUTHORS Vedvick, T.S., Twardzik, D.R. and Dillon, D.C.
TITLE Compounds for immunotherapy and diagnosis of tuberculosis
JOURNAL Patent: EP 1347055-A 17 24-SEP-2003;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
1..1872
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 1.49e-41 Length: 1872
Score: 670.00 Matches: 131
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-4 (1-132) x AX832594 (1-1872)
Qy 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProIle 20
Db 758 ACGCCCGGCTCGGATACCTCCAGCTGTCAGGGTGGCAGGGATTCCGCAATCCGATC 817
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
Db 818 GGGCAGGCGATGGCGATCGCGGGCCAAATCCGATCGGGTGGGGGTCCGCCACCGTTCAT 877
Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyValAlaArg 60
Db 878 ATCGGGCCCTACGGCTTCTCGGCTTGGGTGGTGTTCGACACACACGGCAGCGGCACGA 937
Qy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
Db 938 GTCCAAACGGTGTGGTGGGAGGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGGACGTG 997
Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
Db 998 ATCAGCGGGTGCAGGGGCTCCGATCAACTCGGCCACCGGATGCGGACGCGCTTAAC 1057
Qy 101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
Db 1058 GGGCATCATCCCGGTGACGTATCTCGGTGAACCTGGCAACCAAGTCCGGGGCGCACGGGT 1117
Qy 121 ThrGlyAsnValThrIleuAlaGlnGlyProProAla 132
Db 1118 ACAGGACACGTGACATTCGCGAGGAGACCCCGGCC 1153

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Search completed: April 30, 2004, 02:24:00
Job time : 3854.74 secs

OM protein - nucleic search, using frame plus p2n model

Run on: April 29, 2004, 22:43:07 ; Search time 109.952 Seconds
(without alignments)
1234.209 Million cell updates

Title: US-09-684-215B-17
 Perfect score: 148
 Sequence: 1 TAASDNFOLSQGGGFAIPIGQMAIAGQI 30

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	Delop	6.0
	Delext	7.0

Searched: 2936184 sec. 2261732022 residues

Total number of hits satisfying chosen parameters: 58723368

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
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-FCGAP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DSLOP=6 -DELEXT=7

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Database : Published_Applications_NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	95	95	2	...
3	90	90	3	...
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8	65	65	8	...
9	60	60	9	...
10	55	55	10	...
11	50	50	11	...
12	45	45	12	...
13	40	40	13	...
14	35	35	14	...
15	30	30	15	...
16	25	25	16	...
17	20	20	17	...
18	15	15	18	...
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2	148	100.0	186	9	US-09-849-626-1879	Sequence 1879, Ap
3	148	100.0	186	13	US-10-283-017-1879	Sequence 1879, Ap
4	148	100.0	186	15	US-10-017-754-1879	Sequence 1879, Ap
5	148	100.0	186	15	US-10-113-872-1879	Sequence 1879, Ap
6	148	100.0	399	9	US-09-757-417-46	Sequence 46, Appl
7	148	100.0	399	15	US-10-042-945-46	Sequence 46, Appl
8	148	100.0	447	15	US-10-193-002-4	Sequence 4, Appl
9	148	100.0	447	15	US-10-084-843-4	Sequence 9, Appl
10	148	100.0	447	15	US-10-098-732A-9	Sequence 822, App
11	148	100.0	675	9	US-09-759-143-822	Sequence 822, App
12	148	100.0	675	9	US-09-780-663-822	Sequence 822, App
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14	148	100.0	675	9	US-09-895-793-822	Sequence 822, App
15	148	100.0	675	9	US-09-895-814-822	Sequence 822, App
16	148	100.0	675	14	US-10-018-896-822	Sequence 822, App
17	148	100.0	675	15	US-10-114-678A-822	Sequence 822, App
18	148	100.0	675	15	US-10-294-025-822	Sequence 822, App
19	148	100.0	702	9	US-09-287-843-27	Sequence 27, Appl
20	148	100.0	702	15	US-10-359-460-27	Sequence 27, Appl
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22	148	100.0	822	9	US-09-902-941-1862	Sequence 1862, Ap
23	148	100.0	822	9	US-09-849-626-1862	Sequence 1862, Ap
24	148	100.0	822	13	US-10-283-017-1862	Sequence 1862, Ap
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26	148	100.0	822	15	US-10-113-872-1862	Sequence 1862, Ap
27	148	100.0	861	9	US-09-902-941-1877	Sequence 1877, Ap
28	148	100.0	861	9	US-09-849-626-1877	Sequence 1877, Ap
29	148	100.0	861	13	US-10-283-017-1877	Sequence 1877, Ap
30	148	100.0	861	15	US-10-017-754-1877	Sequence 1877, Ap
31	148	100.0	861	15	US-10-113-872-1877	Sequence 1877, Ap
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35	148	100.0	900	9	US-09-850-716A-353	Sequence 353, App
36	148	100.0	900	9	US-09-897-778-353	Sequence 353, App
37	148	100.0	900	13	US-10-007-700-353	Sequence 353, App
38	148	100.0	900	15	US-10-117-982-353	Sequence 353, App
39	148	100.0	900	16	US-10-313-986-353	Sequence 353, App
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41	148	100.0	915	9	US-09-780-663-834	Sequence 834, App
42	148	100.0	915	9	US-09-822-821-834	Sequence 834, App
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ALIGNMENTS

RESULT 1

US-09-902-941-1879
 ; Sequence 1879, Application US/09902941
 ; Patent No. US20020172952A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Johnson, Jeffrey C.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Marnerakis, Margarita
 ; APPLICANT: Carter, Gary R.
 ; APPLICANT: Faager, Gary R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: McNabb, Andrea
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; OF LUNG CANCER
 ; FILE REFERENCE: 210121.478C17
 ; CURRENT APPLICATION NUMBER: US/09/902,941
 ; CURRENT FILING DATE: 2001-07-10
 ; NUMBER OF SEQ ID NOS: 2002
 ; SOFTWARE: FastSeq for Windows Version 4.0


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; SEQ ID NO 1879
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-1879

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Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
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RESULT 2
US-09-849-626-1879
; Sequence 1879, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1879
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-849-626-1879

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Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

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; Sequence 1879, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
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; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1879
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-017-1879

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Pred. No.: 1.99e-16 Length: 186
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

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; Sequence 1879, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Mamerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1879
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-754-1879

Alignment Scores:
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193.002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072.596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-193-002-4

Alignment Scores:
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Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
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RESULT 9
US-10-084-843-4
Sequence 4, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.

Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-084-843-4

Alignment Scores:
Pred. No.: 5,44e-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-084-843-4 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 11 ACGCCCGCTCCGATAACTCCAGCTGTCACAGGTGGCAGGGATTCCGCATTCGGATC 70

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGCAGCGCATGGCGATCGCGGCCAGATC 100

RESULT 10
US-10-098-732A-9
Sequence 9, Application US/10098732A
Publication No. US20030175294A1
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Corixa Corporation

```

; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Leishmania Antigen
; FILE REFERENCE: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MTB932A (MTB932A
; OTHER INFORMATION: C-terminus)
US-10-098-732A-9

Alignment Scores:
Pred. No.: 5.44e-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-098-732A-9 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 11 ACGGCCGCGTCCGATACTTCAGCTGTCAGGAGGAGGATTCGCCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 71 GGGCAGCGGATGGCGATCGCGGCCAGATC 100

RESULT 11
US-09-759-143-822
; Sequence 822, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurl, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-822

Alignment Scores:
Pred. No.: 8.73e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-098-732A-9 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 11 ACGGCCGCGTCCGATACTTCAGCTGTCAGGAGGAGGATTCGCCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 71 GGGCAGCGGATGGCGATCGCGGCCAGATC 100

RESULT 12
US-09-780-669-822
; Sequence 822, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurl, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-822

Alignment Scores:
Pred. No.: 8.73e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-759-143-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 22 ACGGCCGCGTCCGATACTTCAGCTGTCAGGAGGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 13
```

```

Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-759-143-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 22 ACGGCCGCGTCCGATACTTCAGCTGTCAGGAGGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 12
US-09-780-669-822
; Sequence 822, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurl, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-822

Alignment Scores:
Pred. No.: 8.73e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-780-669-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
DB 22 ACGGCCGCGTCCGATACTTCAGCTGTCAGGAGGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 13
```

US-09-822-827-822
; Sequence 822, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-822

Alignment Scores:
Pred. No.: 8,73e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-822-827-822 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGCGTCCGATAAATTCAGCTGCCAGGCGTGGCAGGATTCCGCATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 14

US-09-895-793-822
; Sequence 822, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-895-793-822

Alignment Scores:
Pred. No.: 8,73e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-895-793-822 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGCGTCCGATAAATTCAGCTGCCAGGCGTGGCAGGATTCCGCATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 15

US-09-895-814-822
; Sequence 822, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-814-822

Alignment Scores:
Pred. No.: 8,73e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-895-814-822 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

Db 22 ACGGCGCGTCCGATTAATCCAGTGTCCAGGTGGCGAGGATTCGCCATTCGATC 81

QY 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
|||||

Db 82 GGGCAGCGGATGCGGATCGCGGCCAGATC 111

RESULT 16

US-10-012-896-822

Sequence 822, Application US/10012896

Publication No. US20020183251A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Kalos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Stolck, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William T.

APPLICANT: Hural, John

APPLICANT: McNeill, Patricia D.

APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals de Bassols, Carlota

APPLICANT: Foy, Teresa

APPLICANT: Fanger, Gary R.

APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C27

CURRENT APPLICATION NUMBER: US/10/012,896

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 1011

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 822

LENGTH: 675

TYPE: DNA

ORGANISM: Homo sapiens

US-10-012-896-822

Alignment Scores:

Pred. No.: 8,73e-16 Length: 675

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-012-896-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
|||||

Db 22 ACGGCGCGTCCGATTAATCCAGTGTCCAGGTGGCGAGGATTCGCCATTCGATC 81

QY 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
|||||

Db 82 GGGCAGCGGATGCGGATCGCGGCCAGATC 111

RESULT 17

US-10-144-678A-822

Sequence 822, Application US/10144678A

Publication No. US20030157089A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolck, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A. W.

APPLICANT: Hepler, William T.

APPLICANT: Hural, John

APPLICANT: McNeill, Patricia D.

APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals y de Bassols, Carlota

APPLICANT: Foy, Teresa M.

APPLICANT: Matanabe, Yoshihiro

APPLICANT: Deng, Ta

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C28

CURRENT APPLICATION NUMBER: US/10/144,678A

CURRENT FILING DATE: 2002-08-12

NUMBER OF SEQ ID NOS: 1033

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 822

LENGTH: 675

TYPE: DNA

ORGANISM: Homo sapiens

US-10-144-678A-822

Alignment Scores:

Pred. No.: 8,73e-16 Length: 675

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-144-678A-822 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
|||||

Db 22 ACGGCGCGTCCGATTAATCCAGTGTCCAGGTGGCGAGGATTCGCCATTCGATC 81

QY 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
|||||

Db 82 GGGCAGCGGATGCGGATCGCGGCCAGATC 111

RESULT 18

US-10-294-025-822

Sequence 822, Application US/10294025

Publication No. US20030185830A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Stolck, John A.

APPLICANT: Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C29

CURRENT APPLICATION NUMBER: US/10/294,025

CURRENT FILING DATE: 2002-11-12

NUMBER OF SEQ ID NOS: 1038

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 822

LENGTH: 675

TYPE: DNA

ORGANISM: Homo sapiens

US-10-294-025-822

Alignment Scores:

Pred. No.: 8.73e-16 Length: 675
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-294-025-822 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
 Db 22 ACGCCGCGTCCGATAACTTCACGCTGTCACAGGGTGGGACGGATTCCGCATCCGATC 81
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 Db 82 GCGCAGGCGATGGCGATCGCGGCGCAGATC 111

RESULT 19

US-09-287-849-27
 ; Sequence 27, Application US/09287849
 ; Patent No. US2002009459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 ; FILE REFERENCE: 014058-009020US
 ; CURRENT APPLICATION NUMBER: US/09/287,849
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 08/818,112
 ; PRIOR FILING DATE: 1997-03-13
 ; PRIOR APPLICATION NUMBER: US 08/942,578
 ; PRIOR FILING DATE: 1997-10-01
 ; PRIOR APPLICATION NUMBER: US 09/025,197
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 09/056,556
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 09/223,040
 ; PRIOR FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 702
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
 ; OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
 ; OTHER INFORMATION: frame 1
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(693)
 ; OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
 ; OTHER INFORMATION: reading frame 1
 ; NAME/KEY: CDS
 ; LOCATION: (2)..(700)
 ; OTHER INFORMATION: reading frame 2
 ; NAME/KEY: CDS
 ; LOCATION: (3)..(701)
 ; OTHER INFORMATION: reading frame 3
 ; OTHER INFORMATION: reading frame 3

Alignment Scores:

Pred. No.: 9.13e-16 Length: 702
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

US-09-287-849-27

DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-287-849-27 (1-702)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProile 20
 Db 25 ACGCCGCGTCCGATAACTTCACGCTGTCACAGGGTGGGACGGATTCCGCATCCGATC 84
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 Db 85 GCGCAGGCGATGGCGATCGCGGCGCAGATC 114

RESULT 20

US-10-359-460-27
 ; Sequence 27, Application US/10359460
 ; Publication No. US2003014791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Alderson, Mark
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
 ; FILE REFERENCE: 014058-009020US
 ; CURRENT APPLICATION NUMBER: US/10/359,460
 ; CURRENT FILING DATE: 2003-02-05
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US/09/287,849
 ; PRIOR FILING DATE: 1997-03-13
 ; PRIOR APPLICATION NUMBER: US 08/818,112
 ; PRIOR FILING DATE: 1997-10-01
 ; PRIOR APPLICATION NUMBER: US 08/942,578
 ; PRIOR FILING DATE: 1997-10-01
 ; PRIOR APPLICATION NUMBER: US 09/025,197
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 09/056,556
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 09/223,040
 ; PRIOR FILING DATE: 1998-12-30
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 702
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
 ; OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading
 ; OTHER INFORMATION: frame 1
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(693)
 ; OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
 ; OTHER INFORMATION: reading frame 1
 ; NAME/KEY: CDS
 ; LOCATION: (2)..(700)
 ; OTHER INFORMATION: reading frame 2
 ; NAME/KEY: CDS
 ; LOCATION: (3)..(701)
 ; OTHER INFORMATION: reading frame 3
 ; OTHER INFORMATION: reading frame 3

Alignment Scores:

Pred. No.: 9.13e-16 Length: 702
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-10-359-460-27

US-09-684-215B-17 (1-30) x US-10-359-460-27 (1-702)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGGAGGATTCCGATTCGGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 85 GGGCAGGCGATGGCGATCGCGGCCAGATC 114

RESULT 21

US-09-736-457-1862

; Sequence 1862, Application US/09736457

; Patent No. US20020168637A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; APPLICANT: Wang, Aijun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736.457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1862

; LENGTH: 822

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-736-457-1862

Alignment Scores:

Pred. No.: 1.09e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-736-457-1862 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGGAGGATTCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 22

US-09-902-941-1862

; Sequence 1862, Application US/09902941

; Patent No. US20020172952A1

; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Tongtong

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Johnson, Jeffrey C.

; APPLICANT: Retter, Marc W.

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Carter, Darick

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C17

; CURRENT APPLICATION NUMBER: US/09/902.941

; CURRENT FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 2002

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1862

; LENGTH: 822

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-902-941-1862

Alignment Scores:

Pred. No.: 1.09e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-902-941-1862 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGGAGGATTCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 23

US-09-849-626-1862

; Sequence 1862, Application US/09849626

; Publication No. US20020197669A1

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya

; APPLICANT: Fanger, Gary

; APPLICANT: Wang, Aijun

; APPLICANT: Wang, Tongtong

; APPLICANT: Switzer, Anne

; APPLICANT: McNeill, Patricia

; APPLICANT: Clapper, Jonathan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C16

; CURRENT APPLICATION NUMBER: US/09/849.626

; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 1926

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1862

; LENGTH: 822

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-849-626-1862

Alignment Scores:

Pred. No.: 1.09e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-849-626-1862 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGGAGGATTCCGATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111


```
RESULT 24
US-10-283-017-1862
; Sequence 1862, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C20
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1862
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-017-1862

Alignment Scores:
Pred. No.: 1,09e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-017-754-1862 (1-822)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGCTGGCGAGGATTCCGCAATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 25
US-10-017-754-1862
; Sequence 1862, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnarakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1862

Alignment Scores:
Pred. No.: 1,09e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-113-872-1862 (1-822)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGCTGGCGAGGATTCCGCAATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 26
US-10-113-872-1862
; Sequence 1862, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C19
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1862
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-113-872-1862

Alignment Scores:
Pred. No.: 1,09e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-017-754-1862 (1-822)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGCTGGCGAGGATTCCGCAATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 27
US-09-902-941-1877
; Sequence 1877, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
```

APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT FILING DATE: 2001-07-10
CURRENT APPLICATION NUMBER: US/09/902.941
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1877
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
US-09-902-941-1877

Alignment Scores:
Pred. No.: 1.15e-15 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-902-941-1877 (1-861)

Qy 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGTTGGCAGGATTCCGCAATCCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGGATGGCGATCGCGGCCAGATC 111

US-09-684-215B-17 (1-30) x US-09-849-626-1877 (1-861)

Qy 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGTTGGCAGGATTCCGCAATCCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGGATGGCGATCGCGGCCAGATC 111

RESULT 29
US-10-283-017-1877
Sequence 1877, Application US/10283017
Publication No. US20030211510A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C20
CURRENT APPLICATION NUMBER: US/10/283.017
CURRENT FILING DATE: 2002-10-28
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1877
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
US-10-283-017-1877

Alignment Scores:
Pred. No.: 1.15e-15 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-283-017-1877 (1-861)

Qy 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGTTGGCAGGATTCCGCAATCCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGGATGGCGATCGCGGCCAGATC 111

RESULT 28
US-09-849-626-1877
Sequence 1877, Application US/09849626
Publication No. US20020197669A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849.626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1877
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
US-09-849-626-1877

Alignment Scores:
Pred. No.: 1.15e-15 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-849-626-1877 (1-861)

Qy 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGTTGGCAGGATTCCGCAATCCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGGATGGCGATCGCGGCCAGATC 111

; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1877
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-754-1877

Alignment Scores:
Pred. No.: 1.15e-15 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-684-215B-17 (1-30) x US-10-017-754-1877 (1-861)

Qy 1 ThrAlaIaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCGATC 111

Search completed: April 30, 2004, 05:10:22
Job time : 111.202 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 22:28:57 ; Search time 15.3589 Seconds

(without alignments)
1083.969 Million cell updates/sec

Title: US-09-684-215B-17

Perfect score: 148

Sequence: 1 TAASDNFLSQGGGFAIPIGQAWAIAQGI 30

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09684215/runat_29042004_061306_13249/app_query.fasta_1.1180
-DB=Issued Patents NA -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09684215@cgn_1_115@runat_29042004_061306_13249 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	100.0	447	3	US-08-818-112-4 Sequence 4, Appli
2	148	100.0	447	4	US-08-818-111-4 Sequence 4, Appli
3	148	100.0	447	4	US-09-056-555-4 Sequence 4, Appli
4	148	100.0	447	4	US-09-072-596-4 Sequence 4, Appli
5	148	100.0	447	4	US-09-072-967-4 Sequence 4, Appli
6	148	100.0	675	4	US-09-636-215-822 Sequence 822, App
7	148	100.0	675	4	US-09-685-166A-822 Sequence 822, App
8	148	100.0	702	4	US-09-287-849-27 Sequence 27, Appli
9	148	100.0	822	4	US-09-736-457-1862 Sequence 1862, Ap
10	148	100.0	900	4	US-09-643-597-353 Sequence 353, App
11	148	100.0	900	4	US-09-606-421B-353 Sequence 353, App
12	148	100.0	915	4	US-09-636-215-834 Sequence 834, App

13	148	100.0	915	4	US-09-685-166A-834 Sequence 834, App
14	148	100.0	945	4	US-09-736-457-1861 Sequence 1861, Ap
15	148	100.0	1012	4	US-09-643-597-351 Sequence 351, App
16	148	100.0	1012	4	US-09-606-421B-351 Sequence 351, App
17	148	100.0	1203	4	US-09-636-215-851 Sequence 851, App
18	148	100.0	1203	4	US-09-685-166A-851 Sequence 851, App
19	148	100.0	1464	4	US-09-620-412C-348 Sequence 348, App
20	148	100.0	1464	4	US-09-598-419-348 Sequence 348, App
21	148	100.0	1557	4	US-09-620-412C-332 Sequence 332, App
22	148	100.0	1557	4	US-09-598-419-332 Sequence 332, App
23	148	100.0	1578	4	US-09-556-877-188 Sequence 188, App
24	148	100.0	1578	4	US-09-620-412C-188 Sequence 188, App
25	148	100.0	1578	4	US-09-598-419-188 Sequence 188, App
26	148	100.0	1752	4	US-09-620-412C-352 Sequence 352, App
27	148	100.0	1752	4	US-09-598-419-352 Sequence 352, App
28	148	100.0	1758	4	US-09-620-412C-336 Sequence 336, App
29	148	100.0	1758	4	US-09-598-419-336 Sequence 336, App
30	148	100.0	1860	4	US-09-620-412C-308 Sequence 308, App
31	148	100.0	1860	4	US-09-598-419-308 Sequence 308, App
32	148	100.0	1872	3	US-08-818-112-17 Sequence 17, Appl
33	148	100.0	1872	4	US-08-818-111-17 Sequence 17, Appl
34	148	100.0	1872	4	US-09-056-556-17 Sequence 17, Appl
35	148	100.0	1872	4	US-09-072-596-17 Sequence 17, Appl
36	148	100.0	1872	4	US-09-072-967-17 Sequence 17, Appl
37	148	100.0	1896	4	US-09-620-412C-324 Sequence 324, App
38	148	100.0	1896	4	US-09-598-419-324 Sequence 324, App
39	148	100.0	1941	4	US-09-620-412C-316 Sequence 316, App
40	148	100.0	1941	4	US-09-598-419-316 Sequence 316, App
41	148	100.0	1965	4	US-09-620-412C-340 Sequence 340, App
42	148	100.0	1965	4	US-09-598-419-340 Sequence 340, App
43	148	100.0	2052	4	US-09-620-412C-356 Sequence 356, App
44	148	100.0	2052	4	US-09-598-419-356 Sequence 356, App
45	148	100.0	2076	4	US-09-620-412C-312 Sequence 312, App

ALIGNMENTS

RESULT 1
US-08-818-112-4
; Sequence 4, Application US/08818112
; Patent No. 6290963
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,112
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C6
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-4

Alignment Scores:
Pred. No.: 5,528-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-684-215B-17 (1-30) x US-08-818-112-4 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 11 ACGGCGGCGTCCGATAAATTCAGCTGCCAGGTTGGCAGGATTCGCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100

RESULT 2

US-08-818-111-4
Sequence 4, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-4

Alignment Scores:

Pred. No.: 5,528-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-08-818-111-4 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 11 ACGGCGGCGTCCGATAAATTCAGCTGCCAGGTTGGCAGGATTCGCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100

RESULT 3

US-09-056-556-4
Sequence 4, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-4

Alignment Scores:

Pred. No.: 5,528-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-056-556-4 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 11 ACGGCGGCGTCCGATAAATTCAGCTGCCAGGTTGGCAGGATTCGCATTCGCATC 70

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QY 21 GlycAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGAGCGGATGGGATCGCGGGCCAGATC 100

RESULT 4
US-09-072-596-4
; Sequence 4, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonia
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 350
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,596
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-072-596-4
Alignment Scores:
Pred. No.: 5.52e-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-072-596-4 (1-447)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGGTCGCGATACTTCACGCTGCCAGGTCGGCAGGATTCGCCATTCGATC 70

RESULT 5
US-09-072-967-4
; Sequence 4, Application US/09072967
; Patent No. 6592877
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hendrickson, Ronald C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TUBERCULOSIS
; NUMBER OF SEQUENCES: 355
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-072-967-4
Alignment Scores:
Pred. No.: 5.52e-16 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-072-967-4 (1-447)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGGTCGCGATACTTCACGCTGCCAGGTCGGCAGGATTCGCCATTCGATC 100

RESULT 6
US-09-636-215-822
; Sequence 822, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Xuqui
; APPLICANT: Henderson, Robert A.
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; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C21
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-822

Alignment Scores:
Pred. No.: 9,28e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-636-215-822 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGCGTCCGATAAATTCAGCTGTCCAGGAGTGGCAGGATTCGCATTCGCATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATCGCATCGCGGCCAGATC 111

RESULT 7
US-09-685-166A-822
; Sequence 822, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 822
; LENGTH: 675
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-822

Alignment Scores:
Pred. No.: 9,28e-16 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-685-166A-822 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGCGTCCGATAAATTCAGCTGTCCAGGAGTGGCAGGATTCGCATTCGCATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATCGCATCGCGGCCAGATC 111

RESULT 8
US-09-287-849-27
; Sequence 27, Application US/09287849
; Patent No. 6627198
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
; TITLE OF INVENTION: and their uses
; FILE REFERENCE: 014058-009020US
; CURRENT APPLICATION NUMBER: US/09/287,849
; CURRENT FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: US 08/818,112
; PRIOR FILING DATE: 1997-03-13
; PRIOR APPLICATION NUMBER: US 08/942,578
; PRIOR FILING DATE: 1997-10-01
; PRIOR APPLICATION NUMBER: US 09/025,197
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 09/056,556
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 09/223,040
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion
; OTHER INFORMATION: Protein Ral2-DPPD (designated Mtb24), reading
; OTHER INFORMATION: frame 1
; NAME/KEY: CDS
; LOCATION: (1)..(693)
; OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
; OTHER INFORMATION: reading frame 1
; NAME/KEY: CDS
; LOCATION: (2)..(700)
; OTHER INFORMATION: reading frame 2
; NAME/KEY: CDS
; LOCATION: (3)..(701)
; OTHER INFORMATION: reading frame 3
US-09-287-849-27

Alignment Scores:
Pred. No.: 9,75e-16 Length: 702
Score: 148.00 Matches:
```

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-287-849-27 (1-702)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGCCCGCGTCCGATACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCATTCGGATC 84
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 85 GGCAGGCGGATGGCGATCGCGGCCAGATC 114

RESULT 9

US-09-736-457-1862

; Sequence 1862, Application US/09736457

; Patent No. 6509448

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; APPLICANT: Wang, Aijun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736.457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1862

; LENGTH: 822

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-736-457-1862

Alignment Scores:

Pred. No.: 1,19e-15 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-736-457-1862 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCCGCGTCCGATACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGGATGGCGATCGCGGCCAGATC 111

RESULT 10

US-09-643-597-353

; Sequence 353, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-643-597-353

Alignment Scores:

Pred. No.: 1,33e-15 Length: 900
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-643-597-353 (1-900)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCCGCGTCCGATACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCATTCGGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGGCGGATGGCGATCGCGGCCAGATC 111

RESULT 11

US-09-606-421B-353

; Sequence 353, Application US/09606421B

; Patent No. 6531315

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606.421B

; CURRENT FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS: 358

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 353

; LENGTH: 900

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-606-421B-353

Alignment Scores:

Pred. No.: 1,33e-15 Length: 900
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-606-421B-353 (1-900)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20


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Db 22 ACGGCGGTCGATAAATTCAGCTGCCAGGTCGGCAGGATTGCCATTCCGATC 81
Qy 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 12
US-09-636-215-834
; Sequence 834, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 834
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-834

Alignment Scores:
Pred. No.: 1.36e-15 Length: 915
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-636-215-834 (1-915)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGTCGATAAATTCAGCTGCCAGGTCGGCAGGATTGCCATTCCGATC 81
Qy 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 13
US-09-685-166A-834
; Sequence 834, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 834
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-834

Alignment Scores:
Pred. No.: 1.36e-15 Length: 915
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-636-215-834 (1-915)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGTCGATAAATTCAGCTGCCAGGTCGGCAGGATTGCCATTCCGATC 81
Qy 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 14
US-09-736-457-1861
; Sequence 1861, Application US/09736457
; Patent No. 8509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1861
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1861

Alignment Scores:
Pred. No.: 1.42e-15 Length: 945
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-685-166A-834 (1-915)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGGTCGATAAATTCAGCTGCCAGGTCGGCAGGATTGCCATTCCGATC 81
Qy 21 GlyAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 14
US-09-736-457-1861
; Sequence 1861, Application US/09736457
; Patent No. 8509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1861
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1861

Alignment Scores:
Pred. No.: 1.42e-15 Length: 945
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
DB: 4 Gaps: 0
```



```
DB: 4 Gaps: 0
US-09-684-215B-17 (1-30) x US-09-636-215-851 (1-1203)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGGTGGCAGGGATTCCGCAATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 18
US-09-685-166A-851
; Sequence 851, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/09/685.166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 851
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-851

Alignment Scores:
Pred. No.: 1,92e-15 Length: 1203
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-685-166A-851 (1-1203)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGGTGGCAGGGATTCCGCAATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 19
US-09-620-412C-348
; Sequence 348, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-348

Alignment Scores:
Pred. No.: 2,47e-15 Length: 1464
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-598-419-348 (1-1464)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGGTGGCAGGGATTCCGCAATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 20
US-09-598-419-348
; Sequence 348, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 348
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-348

Alignment Scores:
Pred. No.: 2,47e-15 Length: 1464
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-598-419-348 (1-1464)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGGTGGCAGGGATTCCGCAATCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 21
US-09-620-412C-332
; Sequence 332, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 332
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-332

Alignment Scores:
Pred. No.: 2,67e-15 Length: 1557
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-620-412C-332 (1-1557)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCGGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 22

US-09-598-419-332
; Sequence 332, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 332
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-332

Alignment Scores:
Pred. No.: 2,67e-15 Length: 1557
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-598-419-332 (1-1557)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCGGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 23

US-09-556-877-188
; Sequence 188, Application US/09556877
; Patent No. 6432916

; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 188
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-188

Alignment Scores:
Pred. No.: 2,71e-15 Length: 1578
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-556-877-188 (1-1578)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCGGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 24

US-09-620-412C-188
; Sequence 188, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 188
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-188

Alignment Scores:
Pred. No.: 2,71e-15 Length: 1578
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-620-412C-188 (1-1578)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCGGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 25
US-09-598-419-188
; Sequence 188, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 188
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-188

Alignment Scores:
Pred. No.: 2,71e-15 Length: 1578
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-598-419-188 (1-1578)

Qy 1 ThrAlaAlaSerAspAnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGATGGCGATCGCGGGCCAGATC 111

RESULT 26
US-09-620-412C-352
; Sequence 352, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 352
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-352

Alignment Scores:
Pred. No.: 3,09e-15 Length: 1752
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-620-412C-352 (1-1752)

Qy 1 ThrAlaAlaSerAspAnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGATGGCGATCGCGGGCCAGATC 111

RESULT 27
US-09-598-419-352
; Sequence 352, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 352
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-352

Alignment Scores:
Pred. No.: 3,09e-15 Length: 1752
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-598-419-352 (1-1752)

Qy 1 ThrAlaAlaSerAspAnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGATGGCGATCGCGGGCCAGATC 111

RESULT 28
US-09-620-412C-336
; Sequence 336, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-336

Alignment Scores:
Pred. No.: 3,11e-15 Length: 1758
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-620-412C-336 (1-1758)

Qy 1 ThrAlaAlaSerAspAnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCCGATC 81

Db 22 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCAGGGATTCCCATTCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

Search completed: April 30, 2004, 05:01:08
Job time : 17.3589 secs

RESULT 29

US-09-598-419-336
; Sequence 336, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-598-419-336

Alignment Scores:
Pred. No.: 3 118-15 Length: 1758
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-598-419-336 (1-1758)

Qy 1 ThrAlaIleAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCGCGTCCGATAAATTCAGCTGTCCAGGGTGGCAGGGATTCCCATTCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 30

US-09-620-412C-308
; Sequence 308, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 308
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-308

Alignment Scores:
Pred. No.: 3 348-15 Length: 1860
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x US-09-620-412C-308 (1-1860)

Qy 1 ThrAlaIleAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 20:32:52 ; Search time 860.167 Seconds

(without alignments)
1511.672 Million cell updates/sec

Title: US-09-684-215B-17

Sequence: 1 TRASNFLSQGGQGFALPFGAMALAQI 30

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO.spool/US09684215/runat_29042004_061304_13185/app_query.fasta_1.1180
-DB=GenEmbl -OFFM=fastap -SUFFIX=rgs -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09684215 @CGN 1 1 6034 @runat_29042004_061304_13185 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*

- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.pod.*
- 36: em.htg.pod.*
- 37: em.htg.vrt.*
- 38: em.htg.vrt.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	148	100.0	186	6	AX369169 Sequence
2	148	100.0	447	6	AR169152 Sequence
3	148	100.0	447	6	AR182442 Sequence
4	148	100.0	447	6	AR194825 Sequence
5	148	100.0	447	6	AR233097 Sequence
6	148	100.0	447	6	AR233302 Sequence
7	148	100.0	447	6	AX423596 Sequence
8	148	100.0	447	6	AX832581 Sequence
9	148	100.0	447	6	BD006325 Compounds
10	148	100.0	447	6	BD006445 Compounds
11	148	100.0	447	6	BD069285 Compounds
12	148	100.0	447	6	BD205817 Compounds
13	148	100.0	675	6	AR261272 Sequence
14	148	100.0	675	6	AR400535 Sequence
15	148	100.0	675	6	AR405802 Sequence
16	148	100.0	675	6	AX201049 Sequence
17	148	100.0	675	6	AX267848 Sequence
18	148	100.0	702	6	BD251334 Fused pro
19	148	100.0	702	6	AR403747 Sequence
20	148	100.0	822	6	AR277645 Sequence
21	148	100.0	822	6	AX369152 Sequence
22	148	100.0	861	6	AX369167 Sequence
23	148	100.0	894	6	AX351489 Sequence
24	148	100.0	900	6	AR220690 Sequence
25	148	100.0	900	6	AX365960 Sequence
26	148	100.0	915	6	AR261281 Sequence
27	148	100.0	915	6	AR400544 Sequence
28	148	100.0	915	6	AR405811 Sequence
29	148	100.0	915	6	AX201061 Sequence
30	148	100.0	915	6	AX267860 Sequence
31	148	100.0	945	6	AR277644 Sequence
32	148	100.0	945	6	AX369151 Sequence
33	148	100.0	1012	6	AR220689 Sequence
34	148	100.0	1012	6	AX365958 Sequence
35	148	100.0	1068	6	BD274032 Sequences
36	148	100.0	1068	6	AX005788 Sequences
37	148	100.0	1143	6	BD274033 Sequences
38	148	100.0	1143	6	AX005790 Sequences
39	148	100.0	1155	6	AX369165 Sequence
40	148	100.0	1203	6	AR400556 Sequence
41	148	100.0	1203	6	AR405823 Sequence
42	148	100.0	1203	6	AX201078 Sequence
43	148	100.0	1203	6	AX267877 Sequence
44	148	100.0	1464	6	AR229410 Sequence
45	148	100.0	1464	6	AR322028 Sequence

ALIGNMENTS

RESULT 1

AX369169 AX369169 186 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 1879 from Patent WO204514.
ACCESSION AX369169
VERSION AX369169.1 GI:18857178
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,
Mannerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S.,
McNabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0204514-A 1879 17-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No.: 4.6e-14 Length: 186
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCGCGTCCGATACCTTCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGGCCAGATC 111
RESULT 2
AR169152 AR169152 447 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 4 from patent US 6290969.
ACCESSION AR169152
VERSION AR169152.1 GI:17906927
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
Vedvick, T.S. and Twardzik, D.R.
TITLE Compounds and methods for immunotherapy and diagnosis of
tuberculosis
JOURNAL Patent: US 6290969-A 4 18-SEP-2001;
FEATURES
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/mol_type="unassigned DNA"
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Pred. No.: 1.18e-13 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR169152 (1-447)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 11 ACGGCGCGTCCGATACCTTCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
RESULT 3
AR182442 AR182442 447 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 4 from patent US 6338852.
ACCESSION AR182442
VERSION AR182442.1 GI:20225649
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,
Vedvick, T.S. and Twardzik, D.R.
TITLE Compounds and methods for diagnosis of tuberculosis
JOURNAL Patent: US 6338852-A 4 15-JAN-2002;
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/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 1.18e-13 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AR182442 (1-447)
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Db 11 ACGGCGCGTCCGATACCTTCAGCTGTCCAGGGTGGCAGGATTCGCCATTCGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGGCCAGATC 100
RESULT 4
AR194825 AR194825 447 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 4 from patent US 6350456.
ACCESSION AR194825
VERSION AR194825.1 GI:20244262
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 447)
AUTHORS Reed, S.G., Skeiky, Y.A.W. and Dillon, D.C.
TITLE Compositions and methods for the prevention and treatment of M.
tuberculosis infection
JOURNAL Patent: US 6350456-A 4 26-FEB-2002;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 1.18e-13 Length: 447
Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR194825 (1-447)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
 Db 11 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCAATTCGATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 71 GGGCAGCGGATGGCGATCGGGCCAGATC 100

RESULT 5

AR233097 LOCUS 447 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 4 from patent US 6458366.
 AR233097 ACCESSION
 AR233097.1 GI:27275533
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 447)

AUTHORS Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,

Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.

TITLE Compounds and methods for diagnosis of tuberculosis

JOURNAL Patent: US 6458366-A 4 01-OCT-2002;

FEATURES Location/Qualifiers

source 1..447

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-13 Length: 447

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR233097 (1-447)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20

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QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 71 GGGCAGCGGATGGCGATCGGGCCAGATC 100

RESULT 6

AR353302 LOCUS 447 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 4 from patent US 6592877.

AR353302 ACCESSION

AR353302.1 GI:33759108

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 447)

AUTHORS Read, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R.,

Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.

TITLE Compounds and methods for immunotherapy and diagnosis of

tuberculosis

JOURNAL Patent: US 6592877-A 4 15-JUL-2003;

FEATURES Location/Qualifiers

source 1..447

/organism="unknown"

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-13 Length: 447

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-13 Length: 447

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR353302 (1-447)

QY 1 ThrAlaAlaSerAspAsnGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20

Db 11 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCAATTCGATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 71 GGGCAGCGGATGGCGATCGGGCCAGATC 100

RESULT 7

AX429596 LOCUS 447 bp DNA linear PAT 21-JUN-2002

DEFINITION Sequence 4 from Patent EP1203817.

AX429596 ACCESSION

AX429596.1 GI:21540845

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1

AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.L.,

Vedvick, T.S. and Twardzik, D.R.

TITLE Compounds and methods for immunotherapy and diagnosis of

tuberculosis

JOURNAL Patent: EP 1203817-A 4 08-MAY-2002;

FEATURES Location/Qualifiers

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/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-13 Length: 447

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Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AX429596 (1-447)

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Db 11 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGGATTCCGCAATTCGATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 71 GGGCAGCGGATGGCGATCGGGCCAGATC 100

RESULT 8

AX832581 LOCUS 447 bp DNA linear PAT 12-DEC-2003

DEFINITION Sequence 4 from Patent EP1347055.

AX832581 ACCESSION

AX832581.1 GI:39840631

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1

AUTHORS Reed, S.G., Skeiky, Y.A., Dillon, D.C., Campos-Neto, A., Houghton, R.,

Vedvick, T.S., Twardzik, D.R., Lodes, M.J., and Hendrickson, R.C.

TITLE Compounds and methods for immunotherapy and diagnosis of

tuberculosis

JOURNAL Patent: US 6592877-A 4 15-JUL-2003;

FEATURES Location/Qualifiers

source 1..447

/organism="unknown"

ORIGIN

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REFERENCE 1
AUTHORS Read,S.G., Skeiky,Y.A., Campos-Neto,A., Houghton,R.L.,
         Vedvick,T.S., Twardzik,D.R. and Dillon,D.C.
TITLE Compounds for immunotherapy and diagnosis of tuberculosis
JOURNAL Patent: EP 1347055-A 4 24-SEP-2003;
        CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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Query Match: 100.00% Indels: 0
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Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100
RESULT 9
BD006325 447 bp DNA linear PAT 31-JAN-2002
LOCUS Compounds and methods for diagnosis of Tuberculosis.
DEFINITION BD006325
ACCESSION BD006325.1 GI:18634696
VERSION JP 2001500383-A/4.
KEYWORDS unidentified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 447)
AUTHORS Read,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R.,
        Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
TITLE Compounds and methods for diagnosis of Tuberculosis
JOURNAL Patent: JP 2001500383-A 4 16-JAN-2001;
        CORIXA CORP
COMMENT OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PF 07-OCT-1997 JP 1998518432
PR 11-OCT-1996 US 08/729622,13-MAR-1997 US 08/818111 PI
STEVEN G REED,YASIR A W SKEIKY,DAVIN C DILLON, PI ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31,C07K14/35,C07K16/12,C12Q1/68,C12N15/62,C01N33/53 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Alignment Scores:
Pred. No.: 1.18e-13 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100
RESULT 10
BD006445 447 bp DNA linear PAT 31-JAN-2002
LOCUS Compounds and methods for immunotherapy and diagnosis of
DEFINITION BD006445
ACCESSION BD006445.1 GI:18634816
VERSION JP 2001501832-A/4.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 447)
AUTHORS Read,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R.,
        Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
TITLE Compounds and methods for immunotherapy and diagnosis of
JOURNAL Patent: JP 2001501832-A 4 13-FEB-2001;
        CORIXA CORP
COMMENT OS Unidentified
PN JP 2001501832-A/4
PD 13-FEB-2001
PF 07-OCT-1997 JP 1998518456
PR 11-OCT-1996 US 08/730510,13-MAR-1997 US 08/818112 PI
STEVEN G REED,YASIR A W SKEIKY,DAVIN C DILLON, PI ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31,C07K14/35,A61K39/04,A61K48/00,A61K49/00,C12N15/62,
C07K13/00,
PC GOIN33/50,GOIN33/60,GOIN33/569,C12N1/19,C12N1/20,C12N1/21, PC
C12N5/10//
PC (C12N1/21,C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..447
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
FEATURES source
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Alignment Scores:
Pred. No.: 1.18e-13 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Db 11 ACGGCGCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGATC 70
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Db 11 ACGGCGCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGATC 70
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100
RESULT 10
BD006445 447 bp DNA linear PAT 31-JAN-2002
LOCUS Compounds and methods for immunotherapy and diagnosis of
DEFINITION BD006445
ACCESSION BD006445.1 GI:18634816
VERSION JP 2001501832-A/4.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 447)
AUTHORS Read,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R.,
        Vedvick,T.S., Twardzik,D.R. and Lodes,M.J.
TITLE Compounds and methods for immunotherapy and diagnosis of
JOURNAL Patent: JP 2001501832-A 4 13-FEB-2001;
        CORIXA CORP
COMMENT OS Unidentified
PN JP 2001501832-A/4
PD 13-FEB-2001
PF 07-OCT-1997 JP 1998518456
PR 11-OCT-1996 US 08/730510,13-MAR-1997 US 08/818112 PI
STEVEN G REED,YASIR A W SKEIKY,DAVIN C DILLON, PI ANTONIO CAMPOS
NETO,
PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK, PI
MICHAEL J LODES
PC C12N15/31,C07K14/35,A61K39/04,A61K48/00,A61K49/00,C12N15/62,
C07K13/00,
PC GOIN33/50,GOIN33/60,GOIN33/569,C12N1/19,C12N1/20,C12N1/21, PC
C12N5/10//
PC (C12N1/21,C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..447
/organism="Unidentified".
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FEATURES source
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Alignment Scores:
Pred. No.: 1.18e-13 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x BD006445 (1-447)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCGCGCTCCGATAACTTCCAGCTGTCCAGGGTGGCGAGGATTCGCCATTCGATC 70
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGGCGATGGCGATCGCGGCCAGATC 100
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Db 71 GGGCAGCGGATGGCGATCGCGGCCAGATC 100

RESULT 11
 BD069285
 LOCUS 447 bp DNA linear PAT 27-AUG-2002
 DEFINITION Compounds and methods for immunotherapy and diagnosis of tuberculosis.
 ACCESSION BD069285
 VERSION 1 GI:22614888
 KEYWORDS JP 2001517069-A/4.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 447)
 AUTHORS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R., Vedvick,T.H. and Twardzik,D.R.
 TITLE Compounds and methods for immunotherapy and diagnosis of tuberculosis.
 JOURNAL Patent: JP 2001517069-A 4 02-OCT-2001;
 COMMENT OS Unidentified
 PN JP 2001517069-A/4
 PD 02-OCT-2001
 PF 30-AUG-1996 JP 1997511464
 PR 01-SEP-1995 US 08/523436,22-SEP-1995 US 08/533634 PR
 22-MAR-1996 US 08/620874,05-JUN-1996 US 08/659683 PR
 12-JUL-1996 US 08/680574
 PI STEVEN G REED,YASIR A W SKEIKY,DAVIN C DILLON,ANTONIO CAMPOS PI NETO,
 PI RAYMOND HOUGHTON,THOMAS H VEDVICK,DANIEL R TWARDZIK PC
 C12N15/31,C07K14/35,A61K38/16,C12N15/62,G01N33/569,C12Q1/68, PC
 C12N5/10,
 PC C12N1/21//A61K39/04, C12N1/21, C12R1:19)
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Compounds and methods for immunotherapy and diagnosis of CC tuberculosis

FEATURES
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 FT key Location/Qualifiers
 FT source 1..447 /organism='Unidentified'.
 Location/Qualifiers
 1..447 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

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 Pred. No.: 1.18e-13 Length: 447
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x BD069285 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 Db 11 ACGGCGCGTCCGATAACTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCGCATC 70
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 Db 71 GGGCAGCGGATGGCGATCGCGGCCAGATC 100

RESULT 12
 BD205817
 LOCUS 447 bp DNA linear PAT 17-JUL-2003
 DEFINITION Compounds and methods for diagnosis of tuberculosis.
 ACCESSION BD205817
 VERSION 1 GI:33015587
 KEYWORDS JP 2002530050-A/4.
 SOURCE Mycobacterium tuberculosis
 ORGANISM Mycobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinobacteriales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 447)
 AUTHORS Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghton,R., Vedvick,T.S., Twardzik,D.R., Lodes,M.J. and Hendrickson,R.C.
 TITLE Compounds and methods for diagnosis of tuberculosis
 JOURNAL Patent: JP 2002530050-A 4 17-SEP-2002;
 COMMENT CORIXA CORP
 OS Mycobacterium tuberculosis
 PN JP 2002530050-A/4
 PD 17-SEP-2002
 PF 17-FEB-1999 JP 2000532132
 PR 18-FEB-1998 US 09/024753,05-MAY-1998 US 09/072596 PI
 STEVEN G REED,YASIR A W SKEIKY,DAVIN C DILLON,ANTONIO CAMPOS PI NETO,
 PI RAYMOND HOUGHTON,THOMAS S VEDVICK,DANIEL R TWARDZIK,MICHAEL J PI LODES,
 PI RONALD C HENDRICKSON
 PC C12N15/09,C07H21/02,C07K21/04,C07K14/35,C07K16/12, PC
 C07K17/00,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/04,C12Q1/ PC
 C07K19/00,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/04,C12Q1/ PC
 68,
 PC G01N33/569,G01N33/68//A61K38/00,A61K39/04,A61K39/395,A61K39/ PC
 395,A61P31/06,
 PC C12N1/21,C12R1:19),C12N15/00,C12N5/00,A61K37/02 CC
 Compounds and methods for diagnosis of tuberculosis. FH Key
 Location/Qualifiers
 FT source 1..447 /organism='Mycobacterium tuberculosis'.
 FT Location/Qualifiers
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 /mol_type='genomic DNA'
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ORIGIN
 Alignment Scores:
 Pred. No.: 1.18e-13 Length: 447
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x BD205817 (1-447)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
 Db 11 ACGGCGCGTCCGATAACTTCAGCTGTCCAGGTTGGCAGGATTCGCCATTCGCATC 70
 Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 Db 71 GGGCAGCGGATGGCGATCGCGGCCAGATC 100

RESULT 13
 AR261272
 LOCUS 675 bp DNA linear PAT 29-JAN-2003
 DEFINITION Sequence 822 from patent US 6321716.
 ACCESSION AR261272
 VERSION AR261272.1 GI:28072035
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 675)
 AUTHORS Mashiki,Z. and Harada,J.
 TITLE Negative pressure control apparatus for engine mounted in vehicle
 JOURNAL Patent: US 6321716-A 822 27-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..675 /organism='unknown'
 /mol_type='genomic DNA'

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ORIGIN
Alignment Scores:
Pred. No.: 1.83e-13 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR261272 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGInGlyGInGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 14
LOCUS AR400535 675 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 822 from patent US 6620922.
ACCESSION AR400535
VERSION AR400535.1 GI:40144000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
COMPOSITIONS and methods for the therapy and diagnosis of prostate cancer
PATENT: US 6620922-A 822 16-SEP-2003;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source
1..675
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.83e-13 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR400535 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGInGlyGInGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 15
LOCUS AR405802 675 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 822 from patent US 6630305.
ACCESSION AR405802
VERSION AR405802.1 GI:40154639
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 675)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
COMPOSITIONS and methods for the therapy and diagnosis of prostate cancer
PATENT: US 6630305-A 822 07-OCT-2003;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source
1..675
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.83e-13 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR405802 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGInGlyGInGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 16
LOCUS AX201049 675 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 679 from Patent WO0151633.
ACCESSION AX201049
VERSION AX201049.1 GI:15390857
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
COMPOSITIONS and methods for the therapy and diagnosis of prostate cancer
PATENT: WO 0151633-A 679 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source
1..675
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/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.83e-13 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AX201049 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGInGlyGInGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 17
LOCUS AX201049 675 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 679 from Patent WO0151633.
ACCESSION AX201049
VERSION AX201049.1 GI:15390857
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
COMPOSITIONS and methods for the therapy and diagnosis of prostate cancer
PATENT: WO 0151633-A 679 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source
1..675
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.83e-13 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AX201049 (1-675)
Qy 1 ThrAlaAlaSerAspAsnPhcInLeuSerGInGlyGInGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGATTCGCCATTCCGATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGCAGCGGATGGCGATCGCGGCCAGATC 111
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Db      82 GGGCAGCGGATCGGCATCGCGGCCAGATC 111
RESULT 17
AX267848
LOCUS   675 bp      DNA      linear      PAT 26-OCT-2001
DEFINITION   Sequence 822 from Patent WO0170332.
ACCESSION   AX267848
VERSION     AX267848.1 GI:16516494
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kaios,M.D., Fager,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
TITLE       Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL     Patent: WO 0170332-A 822 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..675
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.82e-13 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AX267848 (1-675)
Qy      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db      22 ACGCCGCGTCCGATAACTTCCAGCTGCCAGGTCGGCAGGATTCGCCATTCGATC 81
Qy      21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db      82 GGGCAGCGGATCGGCATCGCGGCCAGATC 111
RESULT 18
BD251334
LOCUS   702 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION   Fused protein of Mycobacterium tuberculosis antigen and utilization
thereof.
ACCESSION   BD251334
VERSION     BD251334.1 GI:33061104
KEYWORDS    synthetic construct
SOURCE      artificial construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 702)
AUTHORS     Skeiky,Y.A.W., Alderson,M. and Neto,A.C.
TITLE       Fused protein of Mycobacterium tuberculosis antigen and utilization
thereof
JOURNAL     Patent: JP 2002510494-A 13 09-APR-2002;
CORIXA CORP
COMMENT
OS      Artificial Sequence
PN      JP 2002510494-A/13
PD      09-APR-2002
PF      07-APR-1999 JP 2000542460
PR      07-APR-1998 US 09/056556,30-DEC-1998 US 09/223040 PI
YASIR A W SKEIKY, MARK ALDERSON, ANTONIO CAMPOS NETO PC
C12N15/09, A61K39/04, A61K48/00, A61P31/04, C07K14/35, C07K19/00, PC
C12P21/02
PC      C12N15/00
CC      Description of Artificial Sequence:bi-fusion
protein Ra12-DPPD
CC      (designated)
CC      Mb24), reading frame 1
CC      bi-fusion protein Ra12-DPPD (designated Mb24), reading frame 1
CC      reading frame 2
CC      reading frame 3
FH      Key
FT      CDS
FT      CDS
FT      CDS
FT      CDS
Location/Qualifiers
(1)..(696)
(2)..(700)
(3)..(701)
FEATURES
source
1..702
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1.91e-13 Length: 702
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x BD251334 (1-702)
Qy      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db      25 ACGCCGCGTCCGATAACTTCCAGCTGCCAGGTCGGCAGGATTCGCCATTCGATC 84
Qy      21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db      85 GGGCAGCGGATCGGCATCGCGGCCAGATC 114
RESULT 19
AR403747
LOCUS   702 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION   Sequence 27 from patent US 6627198.
ACCESSION   AR403747
VERSION     AR403747.1 GI:40151423
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 702)
AUTHORS     Reed,S.G., Skeiky,Y.A., Dillon,D.C., Alderson,M. and Campos-Neto,A.
TITLE       Fusion proteins of Mycobacterium tuberculosis antigens and their
uses
JOURNAL     Patent: US 6627198-A 27 30-SEP-2003;
FEATURES
source
1..702
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.91e-13 Length: 702
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AR403747 (1-702)
Qy      1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db      25 ACGCCGCGTCCGATAACTTCCAGCTGCCAGGTCGGCAGGATTCGCCATTCGATC 84
Qy      21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

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Db 85 GGGCAGCGCATGGCGATCGCGGCCAGATC 114

RESULT 20
AR277645

LOCUS 822 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 1862 from patent US 6509448.

ACCESSION AR277645

VERSION AR277645.1 GI:297111294

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 822)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: US 6509448-A 1862 21-JAN-2003;

FEATURES
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Location/Qualifiers
1..822
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/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,26e-13 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR277645 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlnGlyGlnGlyPheAlaIleProIle 20

Db 22 ACGGCGCGCTCCGATAACTTCCAGCTGTCCCGAGGTGGCAGGGATTCGCCATTCGCATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATC 111

RESULT 21
AX369152

LOCUS 822 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 1862 from Patent WO0204514.

ACCESSION AX369152

VERSION AX369152.1 GI:18657170

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W., Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S., Mcnabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.

TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: WO 0204514-A 1862 17-JAN-2002;

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2,26e-13 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR277645 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlnGlyGlnGlyPheAlaIleProIle 20

Db 22 ACGGCGCGCTCCGATAACTTCCAGCTGTCCCGAGGTGGCAGGGATTCGCCATTCGCATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATC 111

RESULT 22
AX369167

LOCUS 861 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 1877 from Patent WO0204514.

ACCESSION AX369167

VERSION AX369167.1 GI:18857177

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W., Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S., Mcnabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.

TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: WO 0204514-A 1877 17-JAN-2002;

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2,38e-13 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AX369167 (1-861)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlnGlyGlnGlyPheAlaIleProIle 20

Db 22 ACGGCGCGCTCCGATAACTTCCAGCTGTCCCGAGGTGGCAGGGATTCGCCATTCGCATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATC 111

RESULT 23
AX351489

LOCUS 894 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 236 from Patent WO0196390.

ACCESSION AX351489

VERSION AX351489.1 GI:18616835

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Jiang, Y., Hepler, W.T., Clapper, J.D., Wang, A. and Secrist, H.

TITLE Compositions and methods for the therapy and diagnosis of colon cancer

JOURNAL Patent: WO 0196390-A 236 20-DEC-2001;

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FEATURES
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CORIXA CORPORATION (US)
  Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
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Alignment Scores:
  Pred. No.: 2,49e-13 Length: 894
  Score: 148.00 Matches: 30
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AX351489 (1-894)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATACTTCCAGTGTCCAGGGTGGCAGGATTGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGCATGGCGATCGCGGGCCAGATC 111
RESULT 24
AR220690 900 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION Sequence 353 from patent US 6426072.
ACCESSION AR220690
VERSION AR220690.1 GI:23327471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 900)
AUTHORS Wang, T., Fan, L., Kalos, M.D., Bangur, C.S., Hosken, N.A., Fanger, G.R.,
Li, S.X., Wang, A., Skeiky, Y.A.W., Henderson, R.A., and McNeill, P.D.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: US 6426072-A 353 30-JUL-2002;
FEATURES
  source
  Location/Qualifiers
    1..900
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
  Pred. No.: 2,49e-13 Length: 900
  Score: 148.00 Matches: 30
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AR220690 (1-900)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATACTTCCAGTGTCCAGGGTGGCAGGATTGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGCATGGCGATCGCGGGCCAGATC 111
RESULT 25
AX365960 900 bp DNA linear PAT 15-FEB-2002
LOCUS
DEFINITION Sequence 353 from Patent WO0200174.
ACCESSION AX365960
VERSION AX365960.1 GI:18697458
KEYWORDS
SOURCE
CORIXA CORPORATION (US)
  Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
ORIGIN
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  Score: 148.00 Matches: 30
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AX365960 (1-900)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATACTTCCAGTGTCCAGGGTGGCAGGATTGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGCATGGCGATCGCGGGCCAGATC 111
RESULT 26
AR261281 915 bp DNA linear PAT 29-JAN-2003
LOCUS
DEFINITION Sequence 834 from patent US 6321716.
ACCESSION AR261281
VERSION AR261281.1 GI:28072044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 915)
AUTHORS Mashiki, Z. and Harada, J.
TITLE Negative pressure control apparatus for engine mounted in vehicle
JOURNAL Patent: US 6321716-A 834 27-NOV-2001;
FEATURES
  source
  Location/Qualifiers
    1..915
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
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  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  DB: 6 Gaps: 0
US-09-684-215B-17 (1-30) x AR261281 (1-915)
QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATACTTCCAGTGTCCAGGGTGGCAGGATTGCCATTCGGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGCATGGCGATCGCGGGCCAGATC 111
```

Db 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 27

AR400544

LOCUS

DEFINITION Sequence 834 from patent US 6620922.

ACCESSION AR400544

VERSION AR400544.1 GI:40144016

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6620922-A 834 16-SEP-2003;

FEATURES

source

1. .915

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2,548-13 Length: 915

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR400544 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20

Db 22 ACGGCGCGGTCCGATACTTCAGCTGCCAGGTGGCGAGGATTCGCCATTCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 28

AR405811

LOCUS

DEFINITION Sequence 834 from patent US 6630305.

ACCESSION AR405811

VERSION AR405811.1 GI:40154648

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6630305-A 834 07-OCT-2003;

FEATURES

source

1. .915

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2,548-13 Length: 915

Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AR400544 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20

Db 22 ACGGCGCGGTCCGATACTTCAGCTGCCAGGTGGCGAGGATTCGCCATTCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 29

AR401061

LOCUS

DEFINITION Sequence 691 from Patent WO0151633.

ACCESSION AR401061

VERSION AR401061.1 GI:15390868

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.

TITLE Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: WO 0151633-A 691 19-JUL-2001;

FEATURES

source

1. .915

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

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Score: 148.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AX201061 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProfile 20

Db 22 ACGGCGCGGTCCGATACTTCAGCTGCCAGGTGGCGAGGATTCGCCATTCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGGATGGCGATCGCGGCCAGATC 111

RESULT 30

AX267860

LOCUS

DEFINITION Sequence 834 from Patent WO0173032.

ACCESSION AX267860

VERSION AX267860.1 GI:16516503

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A.

TITLE Compositions and methods for the therapy and diagnosis of prostate

Cancer

JOURNAL Patent: WO 0173032-A 834 04-OCT-2001;

CORIXA CORPORATION (US)

FEATURES Location/Qualifiers

Source

1..915

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 2.54e-13 Length: 915

Pred. No.: 148.00 Matches: 30

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 100.00% Gaps: 0

DB: 6

US-09-684-215B-17 (1-30) x AX267860 (1-915)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20

Db 22 ACGGCGCGTCCGATAACTTCCAGCTGTCCAGGTTGGCAGGATTCGCCATTCCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATC 111

Search completed: April 30, 2004, 02:24:01

Job time : 861.167 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 22:25:27 ; Search time 587.584 Seconds
(without alignments)
1524.660 Million cell updates/sec

Title: US-09-684-215B-17
Perfect score: 148
Sequence: 1 TAADNFQLSQGGQFAIPGQAWAIAQGI 30

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
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7: em_estio:*
8: em_hic:*
9: gb_est1.*
10: gb_est2.*
11: gb_hic:*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	60	40.5	747	14	CB597827 AGENCOURT
C 2	58	39.2	620	14	CF231012 PtaC0016C
C 3	58	39.2	899	14	CF619317 AGENCOURT
C 4	57	38.5	238	10	BB077789 BB077789
C 5	57	38.5	336	14	CB184974 POPSCO010
C 6	57	38.5	343	14	CA930964 MTU2TA.P1
C 7	57	38.5	351	12	BI070561 C040P04U
C 8	57	38.5	366	12	BI055877 CM3-GN033
C 9	57	38.5	370	14	CA931030 MTU2TA.P1
C 10	57	38.5	370	14	CA931960 MTU2TA.P2
C 11	57	38.5	370	14	CA931997 MTU4TA.P2
C 12	57	38.5	370	14	CA932035 MTU4TA.P2
C 13	57	38.5	370	14	CA932108 MTU4TA.P2
C 14	57	38.5	370	14	CA932138 MTU4TA.P2
C 15	57	38.5	374	14	CA927770 MTU6TR.P1
C 16	57	38.5	374	14	CA928449 MTU6TR.P2
C 17	57	38.5	374	14	CA928493 MTU6TR.P3
C 18	57	38.5	374	14	CA928769 MTU6TR.P6
C 19	57	38.5	384	14	CA931116 MTU2TA.P2
C 20	57	38.5	385	14	CA931394 MTU2TA.P6
C 21	57	38.5	385	14	CA931501 MTU2TA.P8
C 22	57	38.5	387	14	CA931767 MTU4TA.P2
C 23	57	38.5	388	14	CA927636 MTU6TR.P1
C 24	57	38.5	388	14	CA928025 MTU6TR.P1
C 25	57	38.5	388	14	CA929028 MTU6TR.P9
C 26	57	38.5	389	14	CA927727 MTU6TR.P1
C 27	57	38.5	389	14	CA928142 MTU6TR.P1
C 28	57	38.5	390	14	CA927617 MTU6TR.P1
C 29	57	38.5	390	14	CA927744 MTU6TR.P1
C 30	57	38.5	390	14	CA927930 MTU6TR.P1
C 31	57	38.5	402	14	CA933902 MTU3TS.P1
C 32	57	38.5	403	13	B0824075 UB60BPA07
C 33	57	38.5	404	14	CA934515 UB60BPA07
C 34	57	38.5	405	14	CK099325 A062P4.5
C 35	57	38.5	406	14	CF231169 PtaC0018C
C 36	57	38.5	408	14	CA930794 MTU2TA.P1
C 37	57	38.5	409	14	CA931302 MTU2TA.P5
C 38	57	38.5	409	14	CA931312 MTU2TA.P5
C 39	57	38.5	413	14	CA931446 MTU2TA.P7
C 40	57	38.5	413	14	CA931603 MTU2TA.P9
C 41	57	38.5	414	14	CA927769 MTU6TR.P1
C 42	57	38.5	414	14	CA928453 MTU6TR.P2
C 43	57	38.5	414	14	CA929036 MTU6TR.P9
C 44	57	38.5	415	13	B0819016 UA38BPC06
C 45	57	38.5	416	9	A1164854 A069P72u

ALIGNMENTS

RESULT 1
CB597827/c
LOCUS CB597827 747 bp mRNA linear EST 03-APR-2003
DEFINITION AGENCOURT_12972312 NIH_MGC_178 Mus musculus cdna clone
IMAGE:30297156 5', mRNA sequence.
ACCESSION CB597827
VERSION CB597827.1 GI:29515683
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 747)

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Michael Brownstein Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM57 row: j column: 13
 High quality sequence stop: 475.

FEATURES

source

1. .747
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30297156"
 /lab_host="DH10B (TI-phage-resistant)"
 /clone_lib="NIH_MGC_178"
 /note="Organ: lung and heart; Vector: pDNR-LIB; Site 1:
 SfiI (ggccattatggcc); Site 2: SfiI (ggcgctctggcc); cDNA
 made by oligo-dT priming and directionally cloned. 5' and
 3' adaptors were used in cloning as follows:
 5'-AACGCTGCTTCACGACAGATGCGCCGCG-3' and
 5'-ATTCAGAGCGGCGGCGGACATG-dT(30)NN-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 0.5 kb
 size fraction. Library created in the laboratory of M.
 Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 111 Length: 747
 Score: 60.00 Matches: 13
 Percent Similarity: 70.83% Conservatives: 4
 Best Local Similarity: 54.17% Mismatches: 5
 Query Match: 40.54% Indels: 2
 DB: 14 Gaps: 1

US-09-684-215B-17 (1-30) x CB597827 (1-747)

Qy 9 LeuserGinGlyGly-----GlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIle 26
 |||||
 Db 635 TTGGCCAGGTTGGCCATAGGCGAGGTTTCATTGAGCCCTTAGTTCAGGAGTCAACCACA 576
 |||||
 Qy 27 AlaGlyGlnIle 30
 |||||
 Db 575 GCGGGCGAGCTT 564

RESULT 2

CF231012 620 bp mRNA linear EST 05-AUG-2003
 LOCUS
 DEFINITION Ptac0016C2C0206 Poplar cDNA library from cambial zone Populus alba
 x Populus tremula cDNA 5', mRNA sequence.

ACCESSION CF231012
 VERSION CF231012.1 GI:33450441
 KEYWORDS EST.
 SOURCE Populus alba x Populus tremula
 ORGANISM Populus alba x Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 1 (bases 1 to 620)
 DeJardin,A., Lepite,J.-C., Lesage-Descauses,M.-C., Costa,G. and
 Pilate,G.

REFERENCE
 AUTHORS Expressed sequence tags from poplar tension wood tissues - A
 TITLE Comparative analysis from multiple libraries
 JOURNAL Unpublished (2003)
 COMMENT Contact: Lepite JC
 Unit of Forest Improvement, Genetics and Physiology

National Institute for Agricultural Research (INRA)
 Domaine de Linere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
 Tel: 33 02 38 41 78 00
 Fax: 33 02 38 41 78 79
 Email: Jean-Charles.Lepite@leons.inra.fr

PCR Primers
 FORWARD: TriplexA 5' CTGGGAAGCGCCATTGTG 3'
 BACKWARD: TriplexB1 5' ATACGACTCACTATAGGCGCA 3'
 Plate: Ptac0016 row: C column: 2
 Seq primer: TriplexA 5' CTGGGAAGCGCCATTGTG 3'.

FEATURES

source

1. .620
 Location/Qualifiers
 /organism="Populus alba x Populus tremula"
 /mol_type="mRNA"
 /strain="clone INRA 717-1-B4"
 /db_xref="taxon:80863"
 /sex="female"
 /tissue_type="cambial zone harvested on the bark side"
 /dev_stage="3-years-old poplar trees grown in the nursery"
 /clone_lib="Poplar cDNA library from cambial zone"
 /note="A composite cDNA library was made with mRNA
 isolated from opposite and tension wood tissues
 corresponding to the cambial zone collected on the bark
 side after debarking the stem. In this respect, in
 addition to cambium cDNA, this library also contains very
 young phloem and very young xylem cDNA. The sampling was
 done on 3 different tilted trees grown in the nursery.
 cDNA were cloned in an oriented way into SfiI (A and B)
 restriction sites. A one-step conversion of lambda
 Triplex2 to the corresponding Triplex2 plasmid was done
 via site-specific recombination at loxp sites (Clontech;
 SMART cDNA library construction kit). cDNA inserts were
 PCR amplified using flanking primers and then sequenced on
 a ABI3100 Genetic Analyser (Applied Biosystem)"

ORIGIN

Alignment Scores:
 Pred. No.: 174 Length: 620
 Score: 58.00 Matches: 10
 Percent Similarity: 66.67% Conservatives: 6
 Best Local Similarity: 41.67% Mismatches: 8
 Query Match: 39.19% Indels: 0
 DB: 14 Gaps: 0

US-09-684-215B-17 (1-30) x CF231012 (1-620)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuserGinGlyGlyGlnGlyPheAlaIleProIle 20
 |||||
 Db 261 ACATCTGGAGCAGAGGATTCGAGTGTCCAGGAGGATCAGGTTGCATTTCGCA 320
 |||||
 Qy 21 GlyGlnAlaMet 24
 |||||
 Db 321 GGAGAAGTGTATG 332

RESULT 3

CF619317/c 899 bp mRNA linear EST 01-OCT-2003
 LOCUS
 DEFINITION AGENCOURT_15738624 NIH_MGC_219 Homo sapiens cDNA clone
 IMAGE:30523641 5', mRNA sequence.

ACCESSION CF619317
 VERSION CF619317.1 GI:37238006
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 899)

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojiima, Y., Kondo, S., Koya, S., Kurthara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigenoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toyota, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)
UNpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Thermotabolization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kusunagi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tonari, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for further details.

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Location/Qualifiers
1. .238
/organism="Mus musculus"
/mol_type="nrna"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9330145E04"
/sex="male"
/tissue_type="diencephalon"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male
diencephalon"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTATTAATTAATCCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(-) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

```

Best Local Similarity: 45.00% Mismatches: 5
 Query Match: 38.51% Indels: 0
 DB: 10 Gaps: 0

US-09-684-215B-17 (1-30) x BB077789 (1-238)

QY 9 LeuSerGlnGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGly 28
 DB 112 CTGAAGGAGGGGCTCAGGGGATATCAGTCCCAATGGGGAGGCGTCGAAATTAGCGG 53

RESULT 5

CB184974

LOCUS

DEFINITION PopSC00108 Poplar SC cDNA library Populus alba x Populus glandulosa
 cDNA clone PopSC00108, mRNA sequence.

ACCESSION

CB184974

VERSION

CB184974.1 GI:28196969

KEYWORDS

SOURCE

ORGANISM

Populus alba x Populus glandulosa
 Populus alba x Populus glandulosa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE

1 (bases 1 to 336)

AUTHORS

Lee J.S., Lee H.S., Noh E.W. and Choi Y.I.

TITLE

Gene Expression Profiling of the Poplar Suspension Cell

JOURNAL

Unpublished (2003)

COMMENT

Contact: Jae-Soon Lee

Biotechnology Team

Korea Forest Research Institute

44-3 Omockchun-dong, Suwon, 441-350, Korea

Tel: 82 31 290 1162

Fax: 82 31 290 1020

Email: jasolee@foa.go.kr

PCR Primers

FORWARD: T3

BACKWARD: T7

Insert Length: 336

Std Error: 0.00

Seq primer: T3

POLYA-No.

Location/Qualifiers

1..336

/organism="Populus alba x Populus glandulosa"

/mol_type="mRNA"

/db_xref="taxon:153471"

/clone="PopSC00108"

/tissue_type="Suspension cell"

/lab_host="XLL-Blue MRF, strain"

/clone_lib="Poplar SC cDNA library"

/notes="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 111

Score: 57.00

Length: 336

Matches: 10

Percent Similarity: 56.67%

Conservative: 6

Best Local Similarity: 41.67%

Mismatches: 8

Query Match: 38.51%

Indels: 0

Gaps: 0

DB: 14

US-09-684-215B-17 (1-30) x CB184974 (1-336)

QY 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

DB 243 ACATCTGGAGCAGAGGATTCGAAGTGTTCACAGGAGGATCGAGGTTGCAATTTCGCA 302

QY 21 GlyGlnAlaMet 24

DB 303 GGAGAAATGATG 314

RESULT 6

CA930964

LOCUS

343 bp mRNA linear EST 30-DEC-2002

DEFINITION

MTU2TA.PI3.A01 Aspen apex cDNA Library Populus tremuloides cDNA,

mRNA sequence.

ACCESSION

CA930964

VERSION

CA930964.1 GI:27419444

KEYWORDS

EST.

SOURCE

Populus tremuloides (quaking aspen)

ORGANISM

Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE

1 (bases 1 to 343)

AUTHORS

Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and

Tsai,C.-J.

TITLE

Expressed sequence tags from Aspen

JOURNAL

Unpublished (2003)

COMMENT

Contact: Tsai C-J

Plant Biotech Research Center

Michigan Technological University, School of Forest Resources &

Environmental Science

1400 Townsend Drive, Houghton, MI 49931-1295, USA

Tel: 906 487 2914

Fax: 906 487 2915

Email: chtsai@mtu.edu.

Location/Qualifiers

1..343

/organism="Populus tremuloides"

/mol_type="mRNA"

/db_xref="taxon:3693"

/clone_lib="Aspen apex cDNA Library"

/notes="Organ: apex"

ORIGIN

Alignment Scores:

Pred. No.: 114

Score: 57.00

Length: 343

Matches: 10

Percent Similarity: 56.67%

Conservative: 6

Best Local Similarity: 41.67%

Mismatches: 8

Query Match: 38.51%

Indels: 0

Gaps: 0

DB: 14

US-09-684-215B-17 (1-30) x CA930964 (1-343)

QY 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

DB 198 ACATCTGGAGCAGAGGATTCGAAGTGTTCACAGGAGGATCGAGGTTGCAATTTCGCA 257

QY 21 GlyGlnAlaMet 24

DB 258 GGAGAAATGATG 269

RESULT 7

BI070561

LOCUS

DEFINITION

C040P04U Populus strain T89 leaves Populus tremula x Populus

tremuloides cDNA, mRNA sequence.

ACCESSION

BI070561

VERSION

BI070561.1 GI:14491181

KEYWORDS

EST.

SOURCE

Populus tremula x Populus tremuloides

ORGANISM

Populus tremula x Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE

1 (bases 1 to 351)

AUTHORS

Jansson,S., Bhaleera,R., Erlandsson,R., Bjorkbacka,H., Karlsson,J.,

Sterky,F., Gustafsson,P. and Lundberg,J.

TITLE

Gene expression in Populus leaves

JOURNAL

Unpublished (2001)

COMMENT

Contact: Erlandsson R

Department of Biotechnology

Royal Institute of Technology

Teknikringen 30, Stockholm S-10044, Sweden

Tel: 46 8 790 8287

Fax: 46 8 245452
Email: riker@biochem.kth.se.
Location/Qualifiers
source
1. .351

FEATURES

/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/strain="T89"
/db_xref="taxon:47664"
/tissue_type="leaf"
/clone_lib="Populus strain T89 leaves"

ORIGIN

Alignment Scores:
Pred. No.: 117 Length: 351
Score: 57.00 Matches: 10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match: 38.51% Indels: 0
DB: 12 Gaps: 0

US-09-684-215B-17 (1-30) x BI070561 (1-351)

Qy 1 ThrAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

Db 32 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGGAGGATCAGGGTTGGCATTTCTCGCA 91

Qy 21 GlyGlnAlaMet 24

Db 92 GGAGAAATGATG 103

RESULT 8

BI055877
LOCUS CM3-GN0330-120201-735-e08 GN0330 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BI055877
VERSION BI055877.1 GI:14463407
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 366)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

TITLE

sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PubMed

10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM3&t2=CM3-GN0330-120201-735-e08&t3=2001-02-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 366.

FEATURES

source

1. .366
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"

/clone_lib="GN0330"

/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORBESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 124 Length: 366
Score: 57.00 Matches: 10
Percent Similarity: 71.43% Conservative: 5
Best Local Similarity: 47.62% Mismatches: 6
Query Match: 38.51% Indels: 0
DB: 12 Gaps: 0

US-09-684-215B-17 (1-30) x BI055877 (1-366)

Qy 3 AlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIleGlyGln 22

Db 184 GCACCGGAGGAGGACAGCTCGATCGCCCTGGGCAAGGATTCCTGCTGTGGCGGAG 243

Qy 23 Ala 23

Db 244 GCC 246

RESULT 9

CA931030 370 bp mRNA linear EST 30-DEC-2002
LOCUS MTU2TA.PI.A09 Aspen apex cDNA Library Populus tremuloides cDNA,
DEFINITION
ACCESSION CA931030
VERSION CA931030.1 GI:27419510
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE

1 (bases 1 to 370)

AUTHORS

Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Teai, C.-J.

TITLE

Expressed sequence tags from Aspen
Unpublished (2003)
Contact: Teai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2314
Fax: 906 487 2315
Email: chtsai@mtu.edu.

FEATURES

source
1. .370
Location/Qualifiers
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA Library"
/note="Organ: apex"

ORIGIN

Alignment Scores:

Pred. No.: 126 Length: 370
Score: 57.00 Matches: 10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match: 38.51% Indels: 0
DB: 14 Gaps: 0

US-09-684-215B-17 (1-30) x CA931030 (1-370)

Qy	1	ThrAlaAlaSerAspAsn	PheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle	20
Db	146	ACATCTCGACGACAGAGGATT	CGAAGTGTTCGAAGGATCAGGGTTCCGATTCTCGCA	87
Qy	21	GlyClnAlaMet	24	
Db	86	GGAGAAATGATG	75	
RESULT 10				
CA931960				
LOCUS	MTU47A.P25.B07	Aspen apex cDNA Library	Populus tremuloides cDNA,	
DEFINITION		mRNA sequence.		
ACCESSION	CA931960			
VERSION	CA931960.1	GI:27420440		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.			
TITLE	Expressed sequence tags from Aspen			
JOURNAL	Unpublished (2003)			
COMMENT	Plant Biotech Research Center Michigan Technological University, School of Forest Resources & Environmental Science 1400 Townsend Drive, Houghton, MI 49931-1295, USA Tel: 906 487 2914 Fax: 906 487 2915 Email: chtsai@mtu.edu.			
FEATURES				
source				
	1..370			
	/organism="Populus tremuloides"			
	/mol_type="mRNA"			
	/db_xref="taxon:3693"			
	/clone_lib="Aspen apex cDNA library"			
	/note="Organ: apex"			
ORIGIN				
Alignment Scores:				
Pred. No.:	126	Length:	370	
Score:	57.00	Matches:	10	
Percent Similarity:	66.67%	Conservative:	6	
Best Local Similarity:	41.67%	Mismatches:	8	
Query Match:	38.51%	Indels:	0	
DB:	14	Gaps:	0	
US-09-684-215B-17 (1-30) x CA931960 (1-370)				
Qy	1	ThrAlaAlaSerAspAsn	PheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle	20
Db	225	ACATCTCGACGACAGAGGATT	CGAAGTGTTCGAAGGATCAGGGTTCCGATTCTCGCA	284
Qy	21	GlyClnAlaMet	24	
Db	285	GGAGAAATGATG	296	
RESULT 11				
CA931997				
LOCUS	MTU47A.P25.F03	Aspen apex cDNA Library	Populus tremuloides cDNA,	
DEFINITION		mRNA sequence.		
ACCESSION	CA931997			
VERSION	CA931997.1	GI:27420477		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.			
TITLE	Expressed sequence tags from Aspen			
JOURNAL	Unpublished (2003)			
COMMENT	Plant Biotech Research Center Michigan Technological University, School of Forest Resources & Environmental Science 1400 Townsend Drive, Houghton, MI 49931-1295, USA Tel: 906 487 2914 Fax: 906 487 2915 Email: chtsai@mtu.edu.			
FEATURES				
source				
	1..370			
	/organism="Populus tremuloides"			
	/mol_type="mRNA"			
	/db_xref="taxon:3693"			
	/clone_lib="Aspen apex cDNA library"			
	/note="Organ: apex"			
ORIGIN				
Alignment Scores:				
Pred. No.:	126	Length:	370	
Score:	57.00	Matches:	10	
Percent Similarity:	66.67%	Conservative:	6	
Best Local Similarity:	41.67%	Mismatches:	8	
Query Match:	38.51%	Indels:	0	
DB:	14	Gaps:	0	
US-09-684-215B-17 (1-30) x CA931960 (1-370)				
Qy	1	ThrAlaAlaSerAspAsn	PheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle	20
Db	225	ACATCTCGACGACAGAGGATT	CGAAGTGTTCGAAGGATCAGGGTTCCGATTCTCGCA	284
Qy	21	GlyClnAlaMet	24	
Db	285	GGAGAAATGATG	296	
RESULT 11				
CA931997				
LOCUS	MTU47A.P25.F03	Aspen apex cDNA Library	Populus tremuloides cDNA,	
DEFINITION		mRNA sequence.		
ACCESSION	CA931997			
VERSION	CA931997.1	GI:27420477		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.			
TITLE	Expressed sequence tags from Aspen			
JOURNAL	Unpublished (2003)			
COMMENT	Plant Biotech Research Center Michigan Technological University, School of Forest Resources & Environmental Science 1400 Townsend Drive, Houghton, MI 49931-1295, USA Tel: 906 487 2914 Fax: 906 487 2915 Email: chtsai@mtu.edu.			
FEATURES				
source				
	1..370			
	/organism="Populus tremuloides"			
	/mol_type="mRNA"			
	/db_xref="taxon:3693"			
	/clone_lib="Aspen apex cDNA library"			
	/note="Organ: apex"			
ORIGIN				
Alignment Scores:				
Pred. No.:	126	Length:	370	
Score:	57.00	Matches:	10	
Percent Similarity:	66.67%	Conservative:	6	
Best Local Similarity:	41.67%	Mismatches:	8	
Query Match:	38.51%	Indels:	0	
DB:	14	Gaps:	0	
US-				

```

ORIGIN
Alignment Scores:
Pred. No.: 126 Length: 370
Score: 57.00 Matches: 10
Percent Similarity: 66.67% Conservatives: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match: 38.51% Indels: 0
DB: 14 Gaps: 0
/ note="Organ: apex"

US-09-684-215B-17 (1-30) x CA932035 (1-370)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 225 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCGCATTTCGCA 284

QY 21 GlyGlnAlaMet 24
Db 285 GGAGAAATGATG 296

RESULT 13
CA932108
LOCUS
DEFINITION
MTU4TA.P27.A02 Aspen apex cDNA Library Populus tremuloides cDNA,
mRNA sequence.
ACCESSION
CA932108
VERSION
CA932108.1 GI:27420588
KEYWORDS
EST.
SOURCE
Populus tremuloides (quaking aspen)
ORGANISM
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE
1 (bases 1 to 370)
AUTHORS
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Tsai,C.-J.
TITLE
Expressed sequence tags from Aspen
JOURNAL
Unpublished (2003)
COMMENT
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.

FEATURES
source
1..370
Location/Qualifiers
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA Library"
/note="Organ: apex"

ORIGIN
Alignment Scores:
Pred. No.: 126 Length: 370
Score: 57.00 Matches: 10
Percent Similarity: 66.67% Conservatives: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match: 38.51% Indels: 0
DB: 14 Gaps: 0
US-09-684-215B-17 (1-30) x CA932138 (1-370)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 225 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCGCATTTCGCA 284

QY 21 GlyGlnAlaMet 24
Db 285 GGAGAAATGATG 296

RESULT 15
CA927770/c
LOCUS
DEFINITION
MTU6TR.P12.G06 Aspen root cDNA Library Populus tremuloides cDNA,
mRNA sequence.
ACCESSION
CA927770
VERSION
CA927770.1 GI:27416249
KEYWORDS
EST.
SOURCE
Populus tremuloides (quaking aspen)
ORGANISM
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE
1 (bases 1 to 374)
AUTHORS
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Tsai,C.-J.
TITLE
Expressed sequence tags from Aspen
JOURNAL
Unpublished (2003)
COMMENT
Contact: Tsai C-J

```



```

VERSION      CA928769.1  GI:27417250
KEYWORDS     Populus tremuloides (quaking aspen)
SOURCE       Populus tremuloides
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE    1 (bases 1 to 374)
AUTHORS      Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
              Tsai,C.-J.
TITLE        Expressed sequence tags from Aspen
JOURNAL      Unpublished (2003)
COMMENT      Contact: Tsai C-J
              Plant Biotech Research Center
              Michigan Technological University, School of Forest Resources &
              Environmental Science
              1400 Townsend Drive, Houghton, MI 49931-1295, USA
              Tel: 906 487 2914
              Fax: 906 487 2915
              Email: chtsai@mtu.edu.

FEATURES     Location/Qualifiers
              1..374
               /organism="Populus tremuloides"
               /mol_type="mRNA"
               /db_xref="taxon:3693"
               /clone_lib="Aspen root cDNA Library"
               /note="Organ: root"

ORIGIN
Alignment Scores:
Pred. No.:      127      Length:      374
Score:          57.00    Matches:      10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match:    38.51% Indels:      0
DB:             14      Gaps:        0

US-09-684-215B-17 (1-30) x CA928769 (1-374)

Qy 1 ThrAlaAaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 146 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGGAGGATCAGGTTTCGCATTTCGCA 87

Qy 21 GlyGlnAlaMet 24
Db 86 GGAGAAATGATG 75

RESULT 19
CA931116/c
LOCUS        MTU2TA.P2.D03 Aspen apex cDNA Library Populus tremuloides cDNA,
DEFINITION   mRNA sequence.
ACCESSION   CA931116
VERSION     CA931116.1  GI:27419596
KEYWORDS     EST.
SOURCE       Populus tremuloides (quaking aspen)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE    1 (bases 1 to 384)
AUTHORS      Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
              Tsai,C.-J.
TITLE        Expressed sequence tags from Aspen
JOURNAL      Unpublished (2003)
COMMENT      Contact: Tsai C-J
              Plant Biotech Research Center
              Michigan Technological University, School of Forest Resources &
              Environmental Science
              1400 Townsend Drive, Houghton, MI 49931-1295, USA
              Tel: 906 487 2914
              Fax: 906 487 2915
              Email: chtsai@mtu.edu.

FEATURES     Location/Qualifiers
              1..384
               /organism="Populus tremuloides"
               /mol_type="mRNA"
               /db_xref="taxon:3693"
               /clone_lib="Aspen apex cDNA Library"
               /note="Organ: apex"

ORIGIN
Alignment Scores:
Pred. No.:      132      Length:      385
Score:          57.00    Matches:      10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match:    38.51% Indels:      0
DB:             14      Gaps:        0

US-09-684-215B-17 (1-30) x CA931116 (1-384)

Qy 1 ThrAlaAaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 146 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGGAGGATCAGGTTTCGCATTTCGCA 87

Qy 21 GlyGlnAlaMet 24
Db 86 GGAGAAATGATG 75

RESULT 20
CA931394/c
LOCUS        MTU2TA.P6.G03 Aspen apex cDNA Library Populus tremuloides cDNA,
DEFINITION   mRNA sequence.
ACCESSION   CA931394
VERSION     CA931394.1  GI:27419874
KEYWORDS     EST.
SOURCE       Populus tremuloides (quaking aspen)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE    1 (bases 1 to 385)
AUTHORS      Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
              Tsai,C.-J.
TITLE        Expressed sequence tags from Aspen
JOURNAL      Unpublished (2003)
COMMENT      Contact: Tsai C-J
              Plant Biotech Research Center
              Michigan Technological University, School of Forest Resources &
              Environmental Science
              1400 Townsend Drive, Houghton, MI 49931-1295, USA
              Tel: 906 487 2914
              Fax: 906 487 2915
              Email: chtsai@mtu.edu.

FEATURES     Location/Qualifiers
              1..385
               /organism="Populus tremuloides"
               /mol_type="mRNA"
               /db_xref="taxon:3693"
               /clone_lib="Aspen apex cDNA Library"
               /note="Organ: apex"

ORIGIN
Alignment Scores:
Pred. No.:      132      Length:      385
Score:          57.00    Matches:      10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match:    38.51% Indels:      0
DB:             14      Gaps:        0

US-09-684-215B-17 (1-30) x CA931394 (1-385)

Qy 1 ThrAlaAaSerAspAsnPhcInLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

```

```

REFERENCE
AUTHORS Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished (2003)
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.

FEATURES
source Location/Qualifiers
1..387
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA Library"
/note="Organ: apex"

ORIGIN

Alignment Scores:
Pred. No.: 133 Length: 387
Score: 57.00 Matches: 10
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 41.67% Mismatches: 8
Query Match: 38.51% Indels: 0
DB: 14 Gaps: 0

US-09-684-215B-17 (1-30) x CA931767 (1-387)

Qy 1 ThrAlaASeRAspSnPheGlnLeuSerGlnclyGlycAlaIleProIle 20
||||| : ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 242 ACATCGACAGCAGGGATTTCGAAGTGTTCCAAGGAGGATCAGGGTTCCGCA 301

Qy 21 GlyGlnAlaMet 24
||||| ::::: |||||
Db 302 GGAGAAATGATG 313

RESULT 23
CA927636 388 bp mRNA linear EST 30-DEC-2002
LOCUS MTU6TR.F11.C07 Aspen root cDNA Library Populus tremuloides CDNA,
DEFINITION mRNA sequence.
ACCESSION CA927636.1 GI:27416115
VERSION CA927636
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE
AUTHORS Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished (2003)
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.

FEATURES
source Location/Qualifiers
1..388
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

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ORIGIN
Alignment Scores:
Pred. No.: 134
Score: 57.00
Percent Similarity: 66.67%
Best Local Similarity: 41.67%
Query Match: 38.51%
Indels: 14
Gaps: 0
DB:

US-09-684-215B-17 (1-30) x CA927636 (1-388)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 243 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCCGATTCTCCGA 302
Qy 21 GlyGlnAlaMet 24
Db 303 GGAGAAATGATG 314

RESULT 24
CA928025/c
LOCUS
DEFINITION MTU6TR.P15.H06 Aspen root cDNA Library Populus tremuloides cDNA,
ACCESSION CA928025
VERSION CA928025.1 GI:27416504
KEYWORDS mRNA sequence.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 388)
AUTHORS Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Tsai,C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished (2003)
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu
Location/Qualifiers
1..388
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

ORIGIN
Alignment Scores:
Pred. No.: 134
Score: 57.00
Percent Similarity: 66.67%
Best Local Similarity: 41.67%
Query Match: 38.51%
Indels: 14
Gaps: 0
DB:

US-09-684-215B-17 (1-30) x CA928025 (1-388)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 146 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCCGATTCTCCGA 87
Qy 21 GlyGlnAlaMet 24
Db 86 GGAGAAATGATG 75

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Location/Qualifiers
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

ORIGIN
Alignment Scores:
Pred. No.: 134
Score: 57.00
Percent Similarity: 66.67%
Best Local Similarity: 41.67%
Query Match: 38.51%
Indels: 14
Gaps: 0
DB:

US-09-684-215B-17 (1-30) x CA928025 (1-388)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 146 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCCGATTCTCCGA 87
Qy 21 GlyGlnAlaMet 24
Db 86 GGAGAAATGATG 75

TITLE
JOURNAL
COMMENT
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RESULT 25
CA929028/c
LOCUS
DEFINITION MTU6TR.P9.F10 Aspen root cDNA Library Populus tremuloides cDNA,
ACCESSION CA929028
VERSION CA929028.1 GI:27417509
KEYWORDS mRNA sequence.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 388)
AUTHORS Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Tsai,C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished (2003)
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu
Location/Qualifiers
1..388
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

ORIGIN
Alignment Scores:
Pred. No.: 134
Score: 57.00
Percent Similarity: 66.67%
Best Local Similarity: 41.67%
Query Match: 38.51%
Indels: 14
Gaps: 0
DB:

US-09-684-215B-17 (1-30) x CA929028 (1-388)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 146 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCCGATTCTCCGA 87
Qy 21 GlyGlnAlaMet 24
Db 86 GGAGAAATGATG 75

FEATURES
source
1..388
Location/Qualifiers
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

ORIGIN
Alignment Scores:
Pred. No.: 134
Score: 57.00
Percent Similarity: 66.67%
Best Local Similarity: 41.67%
Query Match: 38.51%
Indels: 14
Gaps: 0
DB:

US-09-684-215B-17 (1-30) x CA929028 (1-388)
Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 146 ACATCTGGAGCAGAGGATTCGAAGTGTCCAGAGGATCAGGGTTCCGATTCTCCGA 87
Qy 21 GlyGlnAlaMet 24
Db 86 GGAGAAATGATG 75

TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE ORGANISM
Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eucots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
AUTHORS
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.

TITLE
Expressed sequence tags from Aspen
JOURNAL
COMMENT
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.

FEATURES
source
Location/Qualifiers
1..390
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

ORIGIN

Alignment Scores:	Pred. No.:	Length:
Score:	134	Matches: 390
Percent Similarity:	57.00	Matches: 10
Best Local Similarity:	66.67%	Conservative: 6
Query Match:	41.67%	Mismatches: 8
DB:	38.51%	Indels: 0
	14	Gaps: 0

US-09-684-215B-17 (1-30) x CA927930 (1-390)

QY 1 ThrAlaLaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
146 ACATCTGGAGCAGAGGATTGGAAGTGTTCAGAGGAGATCAGGGTTCCGATTTCGC GA 87

Db 21 GlyGlnAlaMet 24
|||::: |||
86 GGAGAAATGATG 75

Search completed: April 30, 2004, 04:40:53
Job time : 590.584 secs

KEYWORDS
SOURCE ORGANISM
Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eucots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
AUTHORS
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.

TITLE
Expressed sequence tags from Aspen
JOURNAL
COMMENT
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.

FEATURES
source
Location/Qualifiers
1..390
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen root cDNA Library"
/note="Organ: root"

ORIGIN

Alignment Scores:	Pred. No.:	Length:
Score:	134	Matches: 390
Percent Similarity:	57.00	Matches: 10
Best Local Similarity:	66.67%	Conservative: 6
Query Match:	41.67%	Mismatches: 8
DB:	38.51%	Indels: 0
	14	Gaps: 0

US-09-684-215B-17 (1-30) x CA927744 (1-390)

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|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
146 ACATCTGGAGCAGAGGATTGGAAGTGTTCAGAGGAGATCAGGGTTCCGATTTCGC GA 87

Db 21 GlyGlnAlaMet 24
|||::: |||
86 GGAGAAATGATG 75

RESULT 30
CA927930/c
LOCUS MTU6TR.F14.F11 Aspen root cDNA Library Populus tremuloides cDNA,
DEFINITION mRNA sequence.
ACCESSION CA927930
VERSION CA927930.1 GI:27416409
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eucots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
AUTHORS
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai,C-J.

TITLE
Expressed sequence tags from Aspen
JOURNAL
COMMENT
Unpublished (2003)
Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.

FEATURES
Location/Qualifiers

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2004, 20:30:12 ; Search time 85.3349 Seconds
(without alignments)
1493.479 Million cell updates/sec

Title: US-09-684-215B-17
Perfect score: 148
Sequence: 1 TAASDNFQLSGGGFALPIQAWAIAQI 30

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US09684215/runat.29042004.061304.13179/app.query.fasta_1.1180
-DB=N_Geneseq_29Jan04 -QWTF=fastap -SUFFIX=mg -MINMATCH=0.1 -LOEPCI=0
-LOEEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
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-USER=US09684215 @CGN 1.1 819 @runat.29042004.061304.13179 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	186	6 ABK39777	Abk39777 DNA encod
2	148	100.0	186	7 ACA12106	Aca12106 Human His
3	148	100.0	186	7 ACA03292	Aca03292 Lung canc
4	148	100.0	396	4 AAL40769	Aal40769 Nucleotid
5	148	100.0	399	6 ABS71801	Abs71801 Human DNA
6	148	100.0	399	9 AAD60769	Aad60769 Ral2 (s)-
7	148	100.0	447	2 AAT91403	Aat91403 Mycobacte
8	148	100.0	447	2 AAT91466	Aat91466 Mycobacte

9	148	100.0	447	2 AAV44342	Av444342 Mycobacte
10	148	100.0	447	2 AAV64450	Aav64450 M. tuberc
11	148	100.0	447	2 AAZ19040	Aaz19040 M. tuberc
12	148	100.0	447	2 AAZ19252	Aaz19252 M. tuberc
13	148	100.0	447	5 AAS03780	Aas03780 M. tuberc
14	148	100.0	447	6 AAD47080	Aad47080 Mycobacte
15	148	100.0	447	6 AAD28339	Aad28339 Mycobacte
16	148	100.0	672	4 AAL40772	Aal40772 Nucleotid
17	148	100.0	675	4 AAH93896	Aah93896 Ral2-P510
18	148	100.0	675	4 AAS64132	Aas64132 Human /M.
19	148	100.0	675	5 ACA59940	ACA59940 Prostata
20	148	100.0	675	6 ABL95503	Ab195503 Ral2-P51
21	148	100.0	675	7 ACC95667	Acc95667 Prostata
22	148	100.0	675	9 AD314272	Ad314272 Human pro
23	148	100.0	702	2 AAZ20206	Aaz20206 Mycobacte
24	148	100.0	702	4 AAL40770	Aal40770 Nucleotid
25	148	100.0	702	6 ABK14140	Abk14140 DNA encod
26	148	100.0	822	6 ABK39769	Abk39769 DNA encod
27	148	100.0	822	7 ACA12098	ACA12098 Human lun
28	148	100.0	822	7 ACA03284	ACA03284 Lung canc
29	148	100.0	861	6 ABK39776	Abk39776 DNA encod
30	148	100.0	861	7 ACA12105	ACA12105 Human Ral
31	148	100.0	861	7 ACA03291	ACA03291 Lung canc
32	148	100.0	894	6 ABK27798	Abk27798 Human col
33	148	100.0	900	6 AB149257	Ab149257 Ral2/C-te
34	148	100.0	900	6 ABQ92443	Abq92443 Human lun
35	148	100.0	900	8 ADA28443	Ada28443 Lung tumo
36	148	100.0	915	4 AAH93905	Aah93905 Ral2-p775
37	148	100.0	915	4 AAS64141	Aas64141 Human /M.
38	148	100.0	915	5 ACAS9949	Acas9949 Prostata
39	148	100.0	915	5 ABL95512	Ab195512 Ral2-P77
40	148	100.0	915	7 ACC95676	Acc95676 Prostata
41	148	100.0	915	9 ADB14284	Adb14284 Human pro
42	148	100.0	945	6 ABK39768	Abk39768 DNA encod
43	148	100.0	945	7 ACA12097	ACA12097 Human lun
44	148	100.0	945	7 ACA03283	ACA03283 Lung canc
45	148	100.0	1002	6 AAD47078	Aad47078 Mycobacte

ALIGNMENTS

RESULT 1

ABK39777
ID ABK39777 standard; cDNA; 186 BP.

XX AC ABK39777;

XX DT 21-MAY-2002 (first entry)

XX DE DNA encoding Ral2S-L985PEX peptide.

XX KW Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
XX gene; ss.

XX OS Homo sapiens.

XX OS Synthetic;

XX PN W0200204514-A2.

XX PD 17-JAN-2002.

XX PF 10-JUL-2001; 2001WO-US022058.

XX PR 11-JUL-2000; 2000US-00614124.

XX PR 29-AUG-2000; 2000US-00651563.

XX PR 08-SEP-2000; 2000US-00658824.

XX PR 26-SEP-2000; 2000US-00671325.

XX PR 06-OCT-2000; 2000US-00677419.

XX PR 30-OCT-2000; 2000US-00702705.

XX PR 13-DEC-2000; 2000US-00736457.

XX PR 03-MAY-2001; 2001US-00849626.

XX (CORI-) CORIXA CORP.

FA

XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
 PI Marxerakis M, Carter D, Fanger GR, Vedvick JS, Bangur CS, McNabb A;
 PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
 XX WPI: 2002-164634/21.
 DR P-PSDB; AAU85595.
 XX Novel polynucleotide encoding a lung tumor polypeptide useful for
 PT stimulating and/or expanding T cells specific for a tumor protein.
 XX
 XX Claim 1; SEQ ID NO 1879; 223pp; English.
 XX The invention describes an isolated polynucleotide and polypeptide useful
 CC for stimulating and/or expanding T cells specific for a tumor protein
 CC for determining the presence of a cancer in a patient. A composition
 CC containing the polynucleotide and/or polypeptide is useful for treating a
 CC lung cancer in a patient. The polypeptide is useful for removing tumor
 CC cells from a biological sample. The polynucleotide is also useful as
 CC probe or primer to detect the level of mRNA encoding a tumor protein.
 CC This sequence encodes a lung tumor associated protein or protein
 CC fragment, described in the method of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,91e-15 Length: 186
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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 QY 21 GlyGlnLaMetAlaIleAlaGlyGlnIle 30
 Db 82 GGGCAGCGATGGCGATCGCGGCCAGATC 111
 RESULT 2
 ID ACA12106 standard; cDNA; 186 BP.
 XX ACA12106;
 AC
 DT 06-JUN-2003 (first entry)
 XX
 XX Human His-tagged Ral2S-L985PEX fusion protein cDNA.
 DE
 XX Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
 KW T cell expansion; CD4; CD8; Ral2; Gene.
 KW
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX US2002197669-A1.
 XX
 XX 26-DEC-2002.
 PD
 XX 03-MAY-2001; 2001US-00849626.
 XX
 XX 13-DEC-2000; 2000US-00736457.
 XX
 XX (BANG/) BANGUR C S.
 PA (FANG/) FANGER G R.
 PA (WANG/) WANG A.

(WANG/) WANG T.
 PA (SWIT/) SWITZER A P.
 PA (MCNE/) MCNEILL P D.
 PA (CLAP/) CLAPPER J D.
 XX
 PI Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
 PI Clapper JD;
 XX
 DR WPI: 2003-352750/33.
 DR P-PSDB; ABU69570.
 XX
 PT Novel lung cancer polynucleotide encoding lung cancer protein, useful for
 PT detecting the presence of lung cancer in a patient, and in pharmaceutical
 XX compositions, e.g. vaccines, for treating lung cancer.
 XX Example 10; Page; 72pp; English.
 XX The invention relates to a polynucleotide encoding a lung tumour protein,
 CC comprising a sequence selected from any of the 14 sequences mentioned in
 CC the specification, or a sequence (S2) mentioned in specification,
 CC complement of S1, sequences consisting of at least 20 contiguous residues
 CC of S1, sequences that hybridise to S1, sequences having 75%, preferably
 CC 90%, identity to S1, or degenerate variants of S1. Also included are an
 CC isolated polypeptide (comprising a sequence (S3) selected from any one of
 CC the 4 amino acid sequences mentioned in the specification, a sequence
 CC encoded by the polynucleotide, or sequences having at least 70%,
 CC preferably 90%, identity to a sequence encoded by the polynucleotide), an
 CC expression vector comprising the polynucleotide operably linked to an
 CC expression control sequence, a host cell transformed or transfected with
 CC the vector, an isolated antibody (or its antigen-binding fragment) that
 CC specifically binds to the polypeptide, detecting the presence of a cancer
 CC in a patient, a fusion protein comprising the polypeptide, an
 CC oligonucleotide that hybridises to S1 under moderately stringent
 CC conditions, stimulating and/or expanding T cells under moderately stringent
 CC conditions (comprising contacting T cells with the polynucleotide, protein
 CC or antigen-presenting cells, under conditions and for a time sufficient
 CC to permit the stimulation and/or expansion of T cells) and inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the polynucleotide, protein or antigen
 CC presenting cells that express the polynucleotide, such that T cells
 CC proliferate, administering to the patient an effective amount of the
 CC proliferated T cells, and thus inhibiting the development of a cancer in
 CC the patient. The polynucleotide, protein and cells are useful in a
 CC composition for stimulating an immune response in a patient, and for
 CC treating a cancer in a patient (particularly lung cancer). The
 CC oligonucleotide is useful for determining the presence of a cancer in a
 CC patient. The protein and oligonucleotides are useful in pharmaceutical
 CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
 CC or primer for nucleic acid hybridisation, and in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and proteins in tumour cells. An amplified portion of the
 CC polynucleotide is useful for isolating a full-length gene from a suitable
 CC library. The present sequence encodes a fusion protein of human Ral2 with
 CC the protein product of a cDNA (full length, extended or partial) isolated
 CC from a library derived from lung tumour/cancer cells. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from the USPIO at
 CC seqdata.uspto.gov/sequence.html?DocId=20020197669
 XX
 SQ Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,91e-15 Length: 186
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-09-684-215B-17 (1-30) x ACA12106 (1-186)
 QY 1 ThrAlaLaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

DB 22 ACGGCGCGTCCGATTAACCTCCAGCTGTCCAGGTGGCAGGGATTCCGATTCGATC 81
Qy 21 GlycAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGCAGGCGATGCGATCGCGGCCAGATC 111
RESULT 3
ACA03292
ID ACA03292 standard; cDNA; 186 BP.
XX ACA03292;
XX
XX 22-MAY-2003 (first entry)
XX
XX Lung cancer therapy and diagnosis associated cDNA #1767.
XX
XX Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002172952-A1.
XX
XX 21-NOV-2002.
XX
XX 10-JUL-2001; 2001US-00902941.
XX
XX 30-JUN-1999; 99US-00346492.
XX
XX 15-OCT-1999; 99US-00419356.
XX
XX 17-DEC-1999; 99US-00468867.
XX
XX 30-DEC-1999; 99US-00476300.
XX
XX 06-MAR-2000; 2000US-00519642.
XX
XX 22-MAR-2000; 2000US-00533077.
XX
XX 10-APR-2000; 2000US-00546259.
XX
XX 27-APR-2000; 2000US-00560406.
XX
XX 05-JUN-2000; 2000US-00589184.
XX
XX 11-JUL-2000; 2000US-00614124.
XX
XX 29-AUG-2000; 2000US-00651563.
XX
XX 08-SEP-2000; 2000US-00658824.
XX
XX 26-SEP-2000; 2000US-00671325.
XX
XX 06-OCT-2000; 2000US-00677419.
XX
XX 30-OCT-2000; 2000US-00702705.
XX
XX 13-DEC-2000; 2000US-00736457.
XX
XX 03-MAY-2001; 2001US-00849626.
XX
XX (CORI-) CORIXA CORP.
XX
XX Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;
XX Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;
XX WPI; 2003-328427/31.
XX
XX New polynucleotide, useful for preparing a composition for treating or
XX inhibiting development of cancer, e.g. lung cancer.
XX
XX Example 10; SEQID NO 1879; 82pp; English.
XX
XX The invention describes an isolated polynucleotide comprising one of 32
XX sequences, complement or degenerate variants of them. The polynucleotide
XX is useful for preparing a composition e.g. a vaccine or for gene therapy,
XX for treating or inhibiting development of cancer, e.g. lung cancer. This
XX sequence represents a polynucleotide associated with the compositions and
XX methods for the therapy and diagnosis of lung cancer
XX
XX Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2,91e-15 Length: 186
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-17 (1-30) x ACA03292 (1-186)
Qy 1 ThrAlaAlaSerAspIleGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 ACGGCGCGTCCGATTAACCTCCAGCTGTCCAGGTGGCAGGGATTCCGATTCGATC 81
Qy 21 GlycAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGCAGGCGATGCGATCGCGGCCAGATC 111
RESULT 4
AAL40769
ID AAL40769 standard; DNA; 396 BP.
XX AAL40769;
XX
XX 03-OCT-2002 (first entry)
XX
XX Nucleotide sequence encoding Ral2 protein.
XX
XX Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
XX vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
XX immunogen; cytokine; gene; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX CDS 1..396
XX /*tag= a
XX /product= "Ral2 protein"
XX /note= "No start or stop codon"
XX
XX WO200125401-A2.
XX
XX 12-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US027652.
XX
XX 07-OCT-1999; 99US-0158585P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky Y, Guderian J;
XX
XX WPI; 2001-266299/27.
XX
XX P-PSDB; RAO22138.
XX
XX Recombinant nucleic acid molecule for producing high yield expression of
XX desired fusion polypeptides, encodes fusion polypeptide comprising
XX Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
XX
XX Claim 1; Fig 2; 39pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
XX fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
XX kDa C-terminal fragment of serine protease antigen MTB32A of
XX Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
XX The recombinant fusion nucleic acids and polypeptides are useful for
XX providing stable and high yield expression of fusion polypeptides of both
XX eukaryotic and prokaryotic origin and to encode a protein product for use
XX as an antigen for detecting serum antibodies. The presence of serum
XX antibodies to M. tuberculosis antigens in an individual indicates that
XX the individual is infected with it. The fusion polypeptides are useful as
XX sources of proteins for monitoring binding of serum antibodies to fusion
XX proteins and as an immunogen to induce and/or enhance immune responses.
XX The coding sequences can be ligated with a coding sequence of another
XX molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
XX can be used in vivo as a DNA vaccine. This polynucleotide sequence
XX represents the DNA encoding the Ral2 protein
XX
XX Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 U; 0 Other;
XX
Alignment Scores:

Pred. No.: 7.45e-15 Length: 396
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x AAL40769 (1-396)

QY 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 1 ACGGCCGCGTCCGATACTTCCAGCTGCCAGGGTGGCAGGATTGCCATTCGATC 60

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 61 GGGCAGGCGATGGCGATCGCGGCCAGATC 90

RESULT 5

AB571801
ID ABS71801 standard; DNA; 399 BP.

XX AC ABS71801;

XX XX 29-AUG-2003 (revised)

DT 02-DEC-2002 (first entry)

XX Human DNA encoding a mammaglobin/RA12 fusion protein.

XX Human; epitope; mammaglobin; breast cancer; cytostatic; T cell; CD4+;
XX CD8+; antigen; RA12; ds; gene.

XX Homo sapiens.

OS Mycobacterium tuberculosis.

OS Chimeric.

XX WO200253017-A2.

XX 11-JUL-2002.

XX 08-JAN-2002; 2002WO-US003057.

XX 08-JAN-2001; 2001US-00757417.

PR 08-NOV-2001; 2001US-00008045.

XX (CORI-) CORIXA CORP.

XX Fling SP, Foy TM, Clapper JD, Wang A, Johnson JC, Mcneill PD;
PI Sutherland RA;

XX WPI; 2002-706844/76.
DR P-PSDB; ABG94684.

XX Novel polypeptides comprise one or more human mammaglobin epitopes and
PT polynucleotides encoding the polypeptides, useful for preventing and
PT treating breast cancers.

PS Claim 20; Page 115; 121pp; English.

XX The invention relates to an isolated polypeptide (I) comprising 7-30
XX consecutive amino acid residues of human mammaglobin, where one or more
XX mammaglobin-specific T cells specifically reacts with (I). Also included
XX are (1) a composition comprising (I), in combination with a
XX physiologically acceptable carrier or immunostimulant; (2) a diagnostic
XX kit, comprising (I) and a detection reagent comprising a reporter group;
XX (3) removing tumour cells from a biological sample, by contacting a
XX biological sample with T cells that specifically react with (I), under
XX conditions and for a time sufficient to permit the removal of cells
XX expressing mammaglobin or a peptide epitope from the sample; (4) an
XX isolated T cell population (II), comprising T cells prepared using (I);
XX and (5) a composition (C2) comprising a polynucleotide comprising a
XX sequence encoding human mammaglobin (or variant or tagged with an
XX affinity tag), or a polypeptide comprising a human mammaglobin (or
XX variant or tagged with an affinity tag), in combination with an

CC immunostimulant. The peptide is useful for inhibiting the development of
CC breast cancer in a patient, by incubating CD4+ and/or CD8+ T cells
CC isolated from a patient with a mammaglobin epitope, such that T cells
CC proliferate, administering the proliferated T cells to the patient,
CC optionally cloning at least one proliferated T cell and administering at
CC least one cloned cell, and thus inhibiting the development of breast
CC cancer in the patient. The compositions and methods are useful for
CC inhibiting the development of breast cancer in a patient. The present
CC sequence encodes a human mammaglobin/RA12 fusion protein. (Updated on 29-
CC AUG-2003 to standardise OS field)

XX Sequence 399 BP; 109 A; 96 C; 92 G; 102 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.52e-15 Length: 399
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x ABS71801 (1-399)

QY 1 ThrAlaAlaSerAspAsnPhgInLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20
Db 22 ACGGCCGCGTCCGATACTTCCAGCTGCCAGGGTGGCAGGATTGCCATTCGATC 81

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 6

AAD60769
ID AAD60769 standard; DNA; 399 BP.

XX AC AAD60769;

XX 15-JAN-2004 (first entry)

DE RA12 (s)-human MamMFL chimeric DNA construct.

XX Cytostatic; epitope; mammaglobin; mgb; therapy; breast cancer; diagnosis;
KW vaccine; human; chimeric; fusion protein; ds.

XX Chimeric- Homo sapiens.

OS Chimeric- Unidentified.

XX Key Location/Qualifiers
FH CDS 1..399
FT /*tag= a
FT /product= "RA12 (s)-human MamMFL fusion protein"

XX US2002082216-A1.
XX 27-JUN-2002.

XX 08-JAN-2001; 2001US-00757417.
XX 26-MAY-2000; 2000US-00580376.

XX (FANG/) FANGER G R.

XX (FOYT/) FOY T M.

XX (HOUG/) HOUGHTON R L.

XX (REED/) REED S G.

XX Fanger GR, Foy TM, Houghton RL, Reed SG;

XX WPI: 2003-776615/73.

XX P-PSDB; ABW00067.

XX New polypeptide epitopes of human mammaglobin useful in inhibiting
PT development of breast cancer and in breast cancer diagnosis and
PT monitoring, and to produce antibodies also useful in breast cancer

PT therapy, diagnosis and monitoring.
 XX Example 8; Page 29; 66pp; English.

CC The present invention provides polypeptide epitopes of human mamaglobin
 CC (mgb) useful for the therapy, diagnosis and monitoring of breast cancer.
 CC The invention is related to specific epitopes of mamaglobin, to
 CC antibodies and immune cells that recognise such epitopes and to methods
 CC for detecting mamaglobin in patient serum. These peptides, antibodies
 CC and cells may be useful in vaccines and pharmaceutical compositions for
 CC prevention and treatment of breast cancer. The invention is also useful
 CC to detect and/or monitor the progression of breast cancer. The present
 CC sequence is Ra12 (s)-human MamFL chimeric DNA construct used in the
 CC expression of recombinant Ra12(s) MamFL, a fusion protein consisting of
 CC full length human mamaglobin with short Ra12. This protein is used in
 CC the exemplification of the invention

XX Sequence 399 BP; 109 A; 96 C; 92 G; 102 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7,52e-15 Length: 399
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-684-215B-17 (1-30) x AAD60769 (1-399)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 22 ACGGCCGCGTCCGATACCTTCAGCTGCCAGGTGGCAGGATTCGCCATTCGATC 81

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 DB 82 GGGCAGCGATGGCGATCGCGGCCAGATC 111

RESULT 7

ID AAT91403
 AC AAT91403 standard; DNA; 447 BP.

XX AAT91403;

DT 12-JAN-1998 (first entry)

XX Mycobacterium tuberculosis antigen TbrA12 encoding DNA.

XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 KW skin testing; M.tuberculosis; ss.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers
 FH CDS 11..409

FT /*tag= a

FT /product= "Antigen_TbrA12"

PN WO9709429-A2.

PD 13-MAR-1997.

XX 30-AUG-1996; 96WO-US014675.

XX 01-SEP-1995; 95US-00523435.

PR 22-SEP-1995; 95US-00532136.

PR 22-MAR-1996; 96US-00620280.

PR 05-JUN-1996; 96US-00658800.

PR 12-JUL-1996; 96US-00680573.

XX (CORI-) CORIXA CORP.

XX Reed SG, Skeiky YAW, Dallon DC, Campos-Neto A, Houghton R;

PI Vedvick TH, Twardzik DR;

XX WPI; 1997-192904/17.
 DR P-PSDB; AAW32354.

XX New immunogenic polypeptide(s) from soluble M. tuberculosis antigens -
 PT useful for diagnosis of M. tuberculosis infection.

XX Claim 3; Page 49-50; 190pp; English.

CC A new immunogenic polypeptide has been developed comprising an
 CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
 CC variant differing only in conservative substitutions and/or
 CC modifications). The present sequence encodes a specifically claimed
 CC M.tuberculosis antigen, TbrA12. The immunogenic polypeptide can be used
 CC to diagnose M.tuberculosis infection by forming complexes with specific
 CC antibodies in the sample. Fragments of DNA encoding the immunogenic
 CC polypeptide can be used as diagnostic primers or probes and agents that
 CC bind to the antigen, especially monoclonal antibodies or equivalent
 CC polyclonal antibodies, are also used for diagnosis

XX Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 8,66e-15 Length: 447
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-684-215B-17 (1-30) x AAT91403 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 DB 11 ACGGCCGCGTCCGATACCTTCAGCTGCCAGGTGGCAGGATTCGCCATTCGATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

DB 71 GGGCAGCGATGGCGATCGCGGCCAGATC 100

RESULT 8

AAT91466

ID AAT91466 standard; DNA; 447 BP.

XX AAT91466;

XX 07-JAN-1998 (first entry)

XX Mycobacterium tuberculosis antigen TbrA12 encoding DNA.

XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;
 KW skin testing; M.tuberculosis; ss.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers

FT CDS 11..409

FT /*tag= a

FT /product= "Antigen_TbrA12"

PN WO9709428-A2.

PD 13-MAR-1997.

XX 30-AUG-1996; 96WO-US014674.

XX 01-SEP-1995; 95US-00523436.

PR 22-SEP-1995; 95US-00533634.

PR 22-MAR-1996; 96US-00620874.

PR 05-JUN-1996; 96US-00659683.

PR 12-JUL-1996; 96US-00680574.

XX (CORI-) CORIXA CORP.

XX Reed SG, Skeiky YA, Dillon DC, Campos-Neto A, Houghton R;
 PI Vedwick TH, Twardzik DR;
 XX WPI: 1997-192903/17.
 DR P-PSDB; AAV32422.

XX New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
 PT useful in vaccines for prevention or treatment of tuberculosis, also for
 PT diagnosis.

XX Claim 3; Page 50; 168pp; English.

XX A new immunogenic polypeptide has been developed comprising an
 CC immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its
 CC variant differing only in conservative substitutions and/or
 CC modifications). The present sequence encodes a specifically claimed
 CC M. tuberculosis antigen, TbrA12. The immunogenic protein, and fusion
 CC proteins containing one or more of the proteins or one of the proteins
 CC plus ESAT-6, are useful in vaccines, preferably when formulated with a
 CC non-specific adjuvant, to induce an immune response against
 CC M. tuberculosis (for treatment or prevention)

XX SQ Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 8.66e-15 Length: 447
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-684-215B-17 (1-30) x AAT91466 (1-447)

Qy 1 ThrAlaIaSerAspAnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
 Db 11 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGTTGGCAGGATTCGCCATTCGATC 70

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 71 GGGCAGCGATGGCGATCGCGGGCCAGATC 100

RESULT 9

AAV44342
 ID AAV44342 standard; DNA; 447 BP.

XX AAV44342;

XX 17-OCT-2003 (revised)

DT 09-NOV-1998 (first entry)

XX Mycobacterium tuberculosis antigen TbrA12 DNA.

XX Tuberculosis; infection; diagnosis; antigen; TbrA12; ss.

XX Mycobacterium tuberculosis; strain H37Ra.

XX Key Location/Qualifiers

XX CDS 11..406

XX /*tag= a

XX WO9816645-A2.

XX 23-APR-1998.

XX 07-OCT-1997; 97WO-US018214.

XX 11-OCT-1996; 96US-00729622.

XX 13-MAR-1997; 97US-00818111.

XX (CORI-) CORIXA CORP.

XX

XX

XX

XX

XX

XX

XX

XX

XX

PI Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
 XX Vedwick TS, Twardzik DR, Lodes MJ;

XX WPI: 1998-251292/22.

DR P-PSDB; AAV64294.

XX New isolated Mycobacterium tuberculosis polypeptides and DNA - used to
 PT develop products for the detection of M. tuberculosis infection and
 PT diagnosis of tuberculosis.

XX Claim 3; Page 61; 250pp; English.

XX This DNA sequence codes for Mycobacterium tuberculosis soluble antigen
 CC TbrA12 (see AAV64294). It was isolated from a M. tuberculosis strain
 CC H37Ra expression library with rabbit anti-sera raised against M.
 CC tuberculosis supernatant. The invention relates to compositions and
 CC methods for diagnosing tuberculosis. It provides polypeptides (see
 CC AAV64291-W64379) comprising an antigenic portion of a soluble M.
 CC tuberculosis antigen, or an immunogenic portion of an M. tuberculosis
 CC antigen, as well as DNA sequences encoding such polypeptides, recombinant
 CC expression vectors and transformed or transfected host cells. Also
 CC claimed are methods and diagnostic kits for detecting M. tuberculosis
 CC infection in a patient using these polypeptides, antibodies or
 CC oligonucleotide probes and primers, for the diagnosis of tuberculosis.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 8.66e-15 Length: 447
 Score: 148.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-684-215B-17 (1-30) x AAV44342 (1-447)

Qy 1 ThrAlaIaSerAspAnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20

Db 11 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGTTGGCAGGATTCGCCATTCGATC 70

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 71 GGGCAGCGATGGCGATCGCGGGCCAGATC 100

RESULT 10

AAV64450

ID AAV64450 standard; DNA; 447 BP.

XX AAV64450;

XX 27-JAN-1999 (first entry)

DT M. tuberculosis immunogenic polypeptide TbrA12 DNA.

XX Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;

XX vaccine; pharmaceutical; infection; diagnosis; ss.

XX Mycobacterium tuberculosis.

XX WO9816646-A2.

XX 23-APR-1998.

XX 07-OCT-1997; 97WO-US018293.

XX 11-OCT-1996; 96US-00730510.

XX 13-MAR-1997; 97US-00818112.

XX (CORI-) CORIXA CORP.

XX

XX

XX

XX

XX

XX

XX

XX

XX

PI Vedvick TS, Twardzik DR, Lodes MJ;
XX WPI: 1998-261042/23.
DR P-PSDB; AAW81657.
XX Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to
PT develop products for the detection of M. tuberculosis infection and for
PT diagnosis, treatment and prevention of tuberculosis.
XX Claim 3; Page 62-63; 230pp; English.
PS
XX This sequence encodes an immunogenic portion of a soluble Mycobacterium
CC tuberculosis (MT) antigen which can be used in a method for inducing
CC protective immunity against tuberculosis (TB). This sequence can be
CC formulated into vaccines and/or pharmaceutical compositions for
CC immunising against M. tuberculosis infection or may be used for the
CC diagnosis of tuberculosis
XX
SQ Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
Alignment Scores:
Pred. No.: 8.66e-15 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-684-215B-17 (1-30) x AAV64450 (1-447)
QY 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCCGCGTCCGATACACTTCCAGCTGTCCAGGTTGGCAGGGATTCGCCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGCGATGGCGATCGGGGCCAGATC 100
RESULT 11
AAZ19040
ID AAZ19040 standard; DNA; 447 BP.
XX AAZ19040;
XX 05-NOV-1999 (first entry)
XX M. tuberculosis recombinant antigen DNA encoding TbrA12.
XX Antigen; diagnosis; detection; infection; antibody; immunisation;
XX vaccine; immunity; ss.
XX Mycobacterium tuberculosis.
XX W09942118-A2.
XX 26-AUG-1999.
XX 17-FEB-1999; 99WO-US003265.
XX 18-FEB-1998; 98US-00024753.
XX 05-MAY-1998; 98US-00072596.
XX (CORI-) CORIXA CORP.
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI: 1999-527416/44.
XX P-PSDB; AAY38959.
XX New polypeptide comprising antigenic portions of M. tuberculosis.
XX Claim 3; Page 103; 323pp; English.

XX This invention describes novel recombinant antigens and their encoding
CC nucleic acids derived from Mycobacterium tuberculosis. The novel
CC polypeptides are useful for detecting M. tuberculosis infection in a
CC biological sample by detecting antibodies which bind with the
CC polypeptides, and are useful as vaccines for immunizing against M.
CC tuberculosis infection. The new detection methods are needed as current
CC vaccination strategies do not provide 100% immunity
XX
SQ Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
Alignment Scores:
Pred. No.: 8.66e-15 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-684-215B-17 (1-30) x AAZ19040 (1-447)
QY 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 11 ACGGCCGCGTCCGATACACTTCCAGCTGTCCAGGTTGGCAGGGATTCGCCATTCGCATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 71 GGGCAGCGATGGCGATCGGGGCCAGATC 100
RESULT 12
AAZ19252
ID AAZ19252 standard; DNA; 447 BP.
XX AAZ19252;
XX 05-NOV-1999 (first entry)
XX M. tuberculosis antigen TbrA12 DNA sequence.
XX Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
XX immunotherapy; diagnosis; immunisation; vaccine; infection;
XX immune response; skin test; ss.
XX Mycobacterium tuberculosis.
XX W09942076-A2.
XX 26-AUG-1999.
XX 17-FEB-1999; 99WO-US003268.
XX 18-FEB-1998; 98US-00025197.
XX 05-MAY-1998; 98US-00072967.
XX (CORI-) CORIXA CORP.
XX Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Houghton R;
XX Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
XX WPI: 1999-527409/44.
XX P-PSDB; AAY39096.
XX New antigens from Mycobacterium tuberculosis useful in diagnostic skin
XX tests and protective or therapeutic vaccines or compositions.
XX Claim 3; Page 73; 299pp; English.
XX The present invention describes polypeptides comprising an immunogenic
CC part of a Mycobacterium tuberculosis antigen (Ag). Also described are
CC vaccines and fusion protein containing M. tuberculosis Ag's. M.
CC tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other
CC polypeptides fragments, can be used in pharmaceutical compositions or
CC vaccines to generate a protective or therapeutic immune response to M.

CC tuberculosis and as reagents in skin tests for diagnosis of tuberculosis.
CC Ag can induce proliferation of, or cytokine secretion by, T, B or natural
CC killer cells and/or macrophages in tuberculosis-immune subjects. AA219249
CC to AA219460 and AA239083 to AA239225 are used in the exemplification of
CC the present invention

XX Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
SQ

Alignment Scores:
Pred. No.: 8.66e-15 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-684-215B-17 (1-30) x AA219252 (1-447)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 11 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGGTGGCAGGATTCCGCATTCGGATC 70
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 71 GGCAGGCGATGGCGATCGCGGCCAGATC 100

RESULT 13

AA503780
ID AA503780 standard; DNA; 447 BP.

AC AA503780;

XX 29-AUG-2001 (first entry)

DE M. tuberculosis DNA encoding a partial antigen TBRa12.

XX TBRa12; antigen; vaccine; tuberculosis; AIDS;
KW acquired immunodeficiency disease; ss.
XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers
FH CDS 11..409
FT /*tag= a
FT /product= "TBRa12"
FT /partial
FT /note= "No start codon"

XX WO200124820-A1.

XX 12-APR-2001.

XX 10-OCT-2000; 2000WO-US028095.

XX 07-OCT-1999; 99US-0158338P.

XX 07-OCT-1999; 99US-0158425P.

XX (CORI-) CORIXA CORP.

XX Skeiky Y, Reed S, Houghton RL, McNeill PD, Dillon DC, Lodes ML;

XX WPI; 2001-290576/30.

XX P-PSDB; AAU01889.

XX Vaccinating against Mycobacteria infections in mammals using fusion
PT proteins comprising combinations of heterologous antigens.

XX Example 2; Page 162; 168pp; English.

XX The sequence encodes Mycobacterium tuberculosis TBRa12, an M.

CC tuberculosis antigen. Compositions comprising at least 2 heterologous
CC antigens, as a fusion protein, and vectors expressing the fusion proteins
CC are used as vaccines to prophylactically immunise mammals (especially

CC humans) against infection by Mycobacteria. The compositions contain at
CC least 2 heterologous antigens that increase the serological sensitivity
CC of individuals infected with tuberculosis, a disease frequently affecting
CC patients with acquired immunodeficiency disease, AIDS
XX Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;
SQ

Alignment Scores:
Pred. No.: 8.66e-15 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-684-215B-17 (1-30) x AA503780 (1-447)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 11 ACGGCGCGTCCGATAACTTCCAGCTGCCAGGGTGGCAGGATTCCGCATTCGGATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

DB 71 GGCAGGCGATGGCGATCGCGGCCAGATC 100

RESULT 14

AA503780
ID AA503780 standard; DNA; 447 BP.

AC AA503780;

XX 27-JAN-2003 (first entry)

DE Mycobacterium tuberculosis Ra12 antigen encoding DNA.

XX Vaccine; immunity; diagnostic agent; gene therapy; Ra12 antigen; gene;
KW ds.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers
FH CDS 11..409
FT /*tag= a
FT /product= "Ra12 antigenic protein"
FT /note= "No start codon"
FT /partial

XX WO200272792-A2.

XX 19-SEP-2002.

XX 13-MAR-2002; 2002WO-US008223.

XX 13-MAR-2001; 2001US-0275837P.

XX (CORI-) CORIXA CORP.

XX Skeiky Y, Brannon M, Guderian J;

XX WPI; 2002-759844/82.

XX P-PSDB; AA29705.

XX New recombinant nucleic acid molecule comprising a Leishmania TSA, Leif,
PT M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity
PT against pathogenic microorganisms e.g. Leishmania and Mycobacterium
PT tuberculosis.

XX Disclosure; Page 83; 155pp; English.

XX The invention relates to a recombinant nucleic acid molecule encoding a
CC fusion polypeptide. The recombinant nucleic acid comprises a heterologous
CC polynucleotide sequence encoding an antigen or an antigenic fragment from
CC Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a

CC polypeptide or its fragment. The Leishmania polynucleotide is selected
CC from TSA, Leif, M15, and 6H polynucleotides. Sequences of the invention
CC are used in methods for eliciting immune response in mammals. They are
CC useful as vaccines to elicit protective immunity against pathogenic
CC microorganisms such as Leishmania and Mycobacterium tuberculosis, as
CC polypeptides are used for enhancing the expression of polynucleotides, as
CC in vivo diagnostic agents and for raising antibodies in a non-human
CC animal. The invention is used in gene therapy. The present sequence is M.
CC tuberculosis Ra12 (C-terminus of MTB32A; RA35FL) antigen encoding DNA
XX

SQ Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 8.66e-15 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AAD47080 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 11 ACGGCGCGTCCGATACCTCCAGCTGTCACGGTGGCGAGGATTCGCCATTCGCATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 71 GGGCAGCGATGCGATCGCGGCCAGATC 100

RESULT 15

AAD28339
ID AAD28339 standard; cDNA; 447 BP.

XX AAD28339;

DT 22-APR-2002 (first entry)

XX Mycobacterium species MTB32A C-terminal peptide encoding cDNA, MTBRa12.

XX Fusion protein; antigen; serological sensitivity; immune response;

KW tuberculosis; infection; vaccine; MTB32A; Ra32FL; MTBRa12; ss.

OS Mycobacterium sp.

XX Key Location/Qualifiers

PH CDS 11..409

FT /*tag= a

FT /product= "Ra35 protein fragment"

FT /notes= "CDS does not include start codon"

FT /partial

XX WO200198460-A2.

PN 27-DEC-2001.

XX 20-JUN-2001; 2001WO-US019959.

XX 20-JUN-2000; 2000US-00597796.

PR 01-FEB-2001; 2001US-0265737P.

XX (CORI-) CORIXA CORP.

XX Skeiky Y, Reed S, Alderson M;

XX WPI; 2002-147798/19.

DR P-ESDB; AAE17569.

XX Composition comprising MTB39 antigen and MTB32A antigen from

XX Mycobacterium species, useful for eliciting immune response in a subject.

XX Disclosure; Page 99; 136pp; English.

XX

CC The present invention relates to fusion proteins containing at least two
CC Mycobacterium species antigens, nucleotides encoding them and
CC compositions comprising such fusion proteins. The present invention
CC particularly relates to nucleic acids encoding fusion proteins that
CC include two or more individual M. tuberculosis antigens which increase
CC the serological sensitivity of sera from individuals infected with
CC tuberculosis and methods for their use in diagnosis, prevention and
CC treatment of tuberculosis infection. Sequences of the invention are
CC useful for eliciting an immune response in a mammal, e.g., human,
CC immunised with BCG. They are useful in the diagnosis, treatment and
CC prevention of Mycobacterium infection. The fusion proteins and the
CC polynucleotides are useful as diagnostic tools in patients infected with
CC Mycobacterium, in vitro and in vivo assays for detecting humoral
CC antibodies or cell-mediated immunity against M. tuberculosis, for the
CC diagnosis of an infection or monitoring of disease progression, as
CC immunogens to generate or elicit a protective immune response in a
CC patient and for raising anti-M. tuberculosis antibodies in a non-human
CC animal. Sequences of the invention are also used as vaccines. MTB32A
CC fusion proteins of the invention are useful as in vivo diagnostic agents
CC for intradermal skin test. The present sequence is Mycobacterium species
CC MTB32A (Ra32FL) C-terminal protein fragment (residues 244-355) encoding
CC cDNA, MTBRa12

XX SQ Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 8.66e-15 Length: 447
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x AAD28339 (1-447)

QY 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20

DB 11 ACGGCGCGTCCGATACCTCCAGCTGTCACGGTGGCGAGGATTCGCCATTCGCATC 70

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

DB 71 GGGCAGCGATGCGATCGCGGCCAGATC 100

RESULT 16

AAL40772

ID AAL40772 standard; DNA; 672 BP.

XX AAL40772;

AC AAL40772;

XX 06-AUG-2003 (revised)

DT 03-OCT-2002 (first entry)

XX Nucleotide sequence encoding Ra12-mammaglobin fusion protein.

XX Ra12; serine protease antigen; MTB32A; Mycobacterium tuberculosis;

KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;

KW immunogen; cytokine; gene; ds.

XX Mammalia.

OS Unidentified.

OS Chimeric.

XX Key Location/Qualifiers

PH CDS 4..666

FT /*tag= a

FT /product= "Ra12-mammaglobin fusion protein"

XX WO200125401-A2.

PN 12-APR-2001.

XX 06-OCT-2000; 2000WO-US027652.

XX

PR 07-OCT-1999; 99US-0158585P.
XX (CORI-) CORIXA CORP.
XX
PI Skeiky Y, Guderian J;
XX
DR WPI; 2001-266299/27.
DR P-PSDB; RAO22141.
XX
XX Recombinant nucleic acid molecule for producing high yield expression of
PT desired fusion polypeptides, encodes fusion polypeptide comprising
PT Mycobacterium tuberculosis coding sequence and heterologous polypeptide.
XX
PS Disclosure; Fig 5; 39pp; English.
XX
XX The invention relates to a recombinant nucleic acid molecule encoding a
CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
CC kDa C-terminal fragment of serine protease antigen WTB32A of
CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
CC The recombinant fusion nucleic acids and polypeptides are useful for
CC providing stable and high yield expression of fusion polypeptides of both
CC eukaryotic and prokaryotic origin and to encode a protein product for use
CC as an antigen for detecting serum antibodies. The presence of serum
CC antibodies to M. tuberculosis antigens in an individual indicates that
CC the individual is infected with it. The fusion polypeptides are useful as
CC sources of proteins for monitoring binding of serum antibodies to fusion
CC proteins and as an immunogen to induce and/or enhance immune responses.
CC The coding sequences can be ligated with a coding sequence of another
CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
CC can be used in vivo as a DNA vaccine. This polynucleotide sequence
CC represents the DNA encoding the Ral2-mammaglobin fusion protein. (Updated
CC on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 672 BP; 160 A; 185 C; 187 G; 140 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1.44e-14 Length: 672
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x AAL40772 (1-672)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 25 ACGGCCGCGTCCGATAACTTCCAGCTGCCAGGGTGGCAGGATTGCCATTCGCATC 84

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 85 GGGCAGCGCATGGCGATCGCGGCCAGATC 114

RESULT 17
AAH93896
ID AAH93896 standard; cDNA; 675 BP.
XX
AC AAH93896;
XX
DT 04-OCT-2001 (first entry)
XX
DE Ral2-PS10S-C construct cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosstatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX WC200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.
XX (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
XX Claim 8; Page 492-493; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AA01115 to AA01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
XX Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1.45e-14 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-684-215B-17 (1-30) x AAH93896 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCCGCGTCCGATAACTTCCAGCTGCCAGGGTGGCAGGATTGCCATTCGCATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGCATGGCGATCGCGGCCAGATC 111

RESULT 18
AAS64132
ID AAS64132 standard; cDNA; 675 BP.
XX
AC AAS64132;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human /M. tuberculosis Ral2 fusion protein Ral2-PS10S-C cDNA.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
OS Microbacterium; tuberculosis.
OS Synthetic.
OS Chimeric.
XX
XX WC200173032-A2.
XX
PD 04-OCT-2001.
XX


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PF 27-MAR-2001; 2001WO-US0009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 29-AUG-2000; 2000US-00636215.
PR 28-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2001-639232/73.
DR P-PSDB; AAU69899.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
XX Example 17; Page 532; 579pp; English.
XX
XX The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
XX
SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.45e-14 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 4

US-09-684-215B-17 (1-30) x AAS64132 (1-675)
Qy 1 ThrAlaAlaSerAspAenPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGCCGGCTCCGATTAACCTTCACGCTGCCAGGGTGGGAGGATTCGGCATTCGCATC 81
Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGCGATGGCATCGCGGGCCAGATC 111

RESULT 19
ACAS9940
ID ACA59940 standard; cDNA; 675 BP.
XX
XX ACA59940;
AC
XX
XX 10-JUN-2003 (first entry)
DX
XX Prostate cancer therapy associated cDNA #647.
DE
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
XX immunogen; cancer; prostate specific antigen; PSA;
KW

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KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002192763-A1.
XX
XX 19-DEC-2002.
XX
XX 29-JUN-2001; 2001US-00895793.
XX
XX 04-OCT-1999; 99US-0157455P.
XX
XX 04-OCT-2000; 2000US-00679272.
XX
XX 28-MAR-2001; 2001US-00822827.
XX
XX (XUJJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX (HURA/) HURAL J.
XX (MCNE/) MCNEILL P D.
XX (HOUG/) HOUGHTON R L.
XX (DEAS/) Y DE BASSOLS C V.
XX (FOYT/) FOY T M.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
XX WPI; 2001-245062/25.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
XX Example 17; SEQ ID NO 822; 85pp; English.
XX
XX The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
XX Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
SQ

```

```

Alignment Scores:
Pred. No.: 1.45e-14 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 5
DB:

```

US-09-684-215B-17 (1-30) x ACA59940 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTCCAGTGTCCAGGGTGGCAGGATTGCCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGGGGATGGCGATCGCGGCCAGATC 111

RESULT 20

ABL95503
ID ABL95503 standard; cDNA; 675 BP.

AC ABL95503;

DT 29-AUG-2003 (revised)

DT 19-JUL-2002 (first entry)

XX Ra12- P510S-C construct cDNA sequence SEQ ID NO 822.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.

XX Mycobacterium tuberculosis.

OS Homo sapiens.

OS Chimeric.

XX US2002022248-A1.

XX PD 21-FEB-2002.

XX PF 12-JAN-2001; 2001US-00759143.

XX PR 25-FEB-1997; 97US-00806099.

PR 01-AUG-1997; 97US-00904804.

PR 10-FEB-1998; 98US-00020956.

PR 25-FEB-1998; 98US-00030607.

PR 14-JUL-1998; 98US-00115453.

PR 23-SEP-1998; 98US-00159812.

PR 15-JAN-1999; 99US-00232149.

PR 09-APR-1999; 99US-00288946.

PR 13-JUL-1999; 99US-00352616.

PR 12-NOV-1999; 99US-00439313.

PR 18-NOV-1999; 99US-00443686.

PR 14-JAN-2000; 2000US-00483672.

PR 27-MAR-2000; 2000US-00536857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.

PR 13-JUN-2000; 2000US-00593793.

PR 27-JUN-2000; 2000US-00605783.

PR 10-AUG-2000; 2000US-00636215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00657279.

PR 02-OCT-2000; 2000US-00679426.

PR 10-OCT-2000; 2000US-00685166.

XX (XUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.

PA (KALO/) KALOS M D.

PA (FANG/) FANGER G R.

PA (RETT/) RETTER M W.

PA (STOL/) STOLK J A.

PA (DAYC/) DAY C H.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (LISX/) LI S X.

PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;

XX WPI; 2002-255649/30.

XX DR MPI; 2002-255649/30.

XX PT New prostate-specific polynucleotides for diagnosing and treating

PT diseases, in particular prostate cancer, and as markers for the

PT progression of cancer.

XX PT progression of cancer.

XX PS Example 17; SEQ ID NO 822; 87bp; English.

XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)

XX SQ Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1 45e-14 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x ABL95503 (1-675)

Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
Db 22 ACGGCGCGTCCGATAACTCCAGTGTCCAGGGTGGCAGGATTGCCCATTCGGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGGGGATGGCGATCGCGGCCAGATC 111

RESULT 21

ACC95667

ID ACC95667 standard; cDNA; 675 BP.

XX ACC95667;

XX ACC95667;

XX 28-AUG-2003 (first entry)

DT Prostate tumour specific cDNA sequence SEQ ID 822.

XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;

XX immune response; prostate cancer; ss.

XX Homo sapiens.

XX WO200289747-A2.

XX 14-NOV-2002.

XX 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.

XX 29-JUN-2001; 2001US-00895814.

XX 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;

PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;

PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;

PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;

PI Deng T;

```
XX WPI; 2003-167130/16.
DR
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX
XX Example 17; Page 601-602; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.45e-14 Length: 675
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-09-684-215B-17 (1-30) x ACC95667 (1-675)
QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
Db 22 ACGGCGCGTCCGATACTTCAGCTGCCAGGGTGGCAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
Db 82 GGGCAGCGCATGGCGATCGCGGGCGAGATC 111
RESULT 22
ADBI4272
ID ADBI4272 standard; cDNA; 675 BP.
XX
AC ADBI4272;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific protein P510S-RAL2 construct C cDNA.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell; gene; fusion protein.
XX
OS Chimeric.
OS Homo sapiens.
OS Mycobacterium tuberculosis.
XX
XX US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
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PR 14-JAN-2000; 2000US-00483672.
PR 17-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709739.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX (CORI-) CORIXA CORP.
PA
XX Xu J, Stolk JA, Kalos MD;
PI WPI; 2003-756193/71.
XX P-PSDB; ADBI4275.
DR
DR
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 17; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody for antigen binding
CC fragment that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a cDNA encoding a
CC fusion protein comprising a prostate specific protein. Note: Except where
CC otherwise indicated, the sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
XX Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.45e-14 Length: 675
Score: 148.00 Matches: 30
```

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9
DB: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-684-215B-17 (1-30) x ADB14272 (1-675)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProile 20
DB 22 ACGGCGCGTCCGATTAACCTCCAGCTGTCCAGGCTGGGAGGATTCGCATTCGCATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGATGCGGATCGCGGCGCGATC 111

RESULT 23

AAZ20206
ID AAZ20206 standard; DNA; 702 BP.

XX
AC AAZ20206;

XX 17-JAN-2000 (first entry)

XX Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA.
DE Tuberculosis; antigen; fusion protein; Mtb24; Ral2; DPPD; diagnosis;
KW therapy; vaccine; immunogen; ss.

XX Mycobacterium tuberculosis.

XX WO9951748-A2.

XX 14-OCT-1999.

XX 07-APR-1999; 99WO-US007717.

XX 07-APR-1998; 98US-00056556.

XX 30-DEC-1998; 98US-00223040.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Alderson M, Campos-Neto A;

XX WPI; 1999-601610/51.

XX P-PSDB; AAY32071.

XX New fusion proteins useful for diagnosis, prevention and treatment of

XX tuberculosis.

XX Example; Fig 13A-B; 83pp; English.

XX This DNA sequence includes a coding region for a recombinant
CC Mycobacterium tuberculosis bi-antigen fusion protein (see AAY32071),
CC termed Mtb24, composed of the antigens Ral2 and DPPD. The DNA is useful
CC for the recombinant production of the fusion protein. Coding sequences
CC for the antigens were modified by PCR in order to facilitate their fusion
CC and subsequent expression of the fusion protein, and then ligated. The
CC invention provides fusion proteins (see AAY32053-71) containing at least
CC 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides
CC encoding them are useful as vaccines for preventing tuberculosis
CC (claimed), for diagnosis (via in vitro assays or intradermal skin tests
CC for detection of anti-M. tuberculosis antibodies), monitoring of disease
CC progression, and treatment of tuberculosis. They are more effective
CC immunogens than mixtures of the individual protein components

XX Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-52e-14 Length: 702
Score: 148.00 Matches: 30
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0

DB: 2 Gaps: 0

US-09-684-215B-17 (1-30) x AAZ20206 (1-702)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyGlnGlyPheAlaIleProile 20
DB 25 ACGGCGCGTCCGATTAACCTCCAGCTGTCCAGGCTGGGAGGATTCGCATTCGCATC 84

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

DB 85 GGGCAGCGATGCGGATCGCGGCGCGATC 114

RESULT 24

RAA40770

ID AAL40770 standard; DNA; 702 BP.

XX
AC AAL40770;

XX 03-OCT-2002 (first entry)

XX Nucleotide sequence encoding Ral2-DPPD fusion protein.

XX Ral2; serine protease antigen; Mtb32A; Mycobacterium tuberculosis;
KW vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
KW immunogen; cytokine; gene; ds.

XX Unidentified.

XX Chimeric.

XX Key Location/Qualifiers

XX CDS 4..696

XX /tag= a

XX /product= "Ral2-DPPD fusion protein"

XX WO200125401-A2.

XX 12-APR-2001.

XX 06-OCT-2000; 2000WO-US027652.

XX 07-OCT-1999; 99US-0158585P.

XX (CORI-) CORIXA CORP.

XX Skeiky Y, Guderian J;

XX WPI; 2001-266299/27.

XX P-PSDB; AAO22139.

XX Recombinant nucleic acid molecule for producing high yield expression of

XX desired fusion polypeptides, encodes fusion polypeptide comprising

XX Mycobacterium tuberculosis coding sequence and heterologous polypeptide.

XX Example 1; Fig 3; 39pp; English.

XX The invention relates to a recombinant nucleic acid molecule encoding a
CC fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
CC kDa C-terminal fragment of serine protease antigen Mtb32A of
CC Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.
CC The recombinant fusion nucleic acids and polypeptides are useful for
CC providing stable and high yield expression of fusion polypeptides of both
CC eukaryotic and prokaryotic origin and to encode a protein product for use
CC as an antigen for detecting serum antibodies. The presence of serum
CC antibodies to M. tuberculosis antigens in an individual indicates that
CC the individual is infected with it. The fusion polypeptides are useful as
CC sources of proteins for monitoring binding of serum antibodies to fusion
CC proteins and as an immunogen to induce and/or enhance immune responses.
CC The coding sequences can be ligated with a coding sequence of another
CC molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and
CC can be used in vivo as a DNA vaccine. This polynucleotide sequence
CC represents the DNA encoding the Ral2-DPPD fusion protein

XX Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;

PR	01-OCT-1997;	97US-00942578.
PR	18-FEB-1998;	98US-00025197.
PR	07-APR-1998;	98US-00056556.
PR	30-DEC-1998;	98US-00223040.
XX	(REED/) REED S G.	
PA	(SKEI/) SKEIKY Y A.	
PA	(DILL/) DILLON D C.	
FA	(ALDE/) ALDERSON M.	
PA	(CAMP/) CAMPOS-NETO A.	
XX		
XX	Reed SG, Skeiky YA, Dillon DC, Alderson M, Campos-Neto A;	
PI		
XX		
XX		
DR	WPI: 2002-171134/22.	
DR	P-PSDB; AAU74600, AAU76541, AAU76542.	
XX		
XX	New fusion proteins of Mycobacterium tuberculosis antigens, useful for	
PT	diagnosing, treating or preventing M. tuberculosis infection,	
PT	particularly as vaccine for treating or preventing tuberculosis.	
XX		
XX	Example; Fig 13; 62pp; English.	
PS		
XX		
CC	The invention relates to a purified polypeptide which induces an immune	
CC	response of Mycobacterium tuberculosis. Polypeptides of the invention are	
CC	useful for diagnosing, treating or preventing M. tuberculosis infection,	
CC	particularly tuberculosis infection. In particular, the polypeptides are	
CC	useful as a vaccine formulation with an adjuvant to afford long-term	
CC	protection in animals against the development of tuberculosis. The	
CC	protein coding sequence may be used to encode a protein product for use	
CC	as an immunogen to induce and/or enhance an immune response to M.	
CC	tuberculosis. This sequence represents DNA encoding an M. tuberculosis	
CC	fusion protein of the invention. This polynucleotide encodes 3 different	
CC	proteins, each in a different reading frame. (Updated on 29-AUG-2003 to	
CC	standardise OS field)	
XX		
SQ	Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 U; 0 Other;	
Alignment Scores:		
Score:	1.52e-14	Length: 702
Pred. No.:	148.00	Matches: 30
Score:	100.00%	Conservative: 0
Percent Similarity:	100.00%	Mismatches: 0
Best Local Similarity:	100.00%	Indels: 0
Query Match:	100.00%	Gaps: 0
DB:	6	
US-09-684-215B-17 (1-30) x ABK14140 (1-702)		
QY	1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20	
Db	25 ACGGCCGCGTCCGATAACTTCCAGCTGTCCAGGGTGGCAGGGATTCGCCATTCGATC 84	
QY	21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30	
Db	85 GGCAGCGCATGGCGATCGCGGCCAGATC 114	
RESULT 26		
ABK14140		
ID	ABK14140 standard; DNA; 702 BP.	
XX		
AC	ABK14140;	
XX		
XX	29-AUG-2003 (revised)	
DT	08-MAY-2002 (first entry)	
XX		
XX	DNA encoding antigenic fusion protein Ral2-DPPD (Mtb24).	
DE		
XX		
KW	Fusion protein; tuberculosis; Mycobacterium tuberculosis; gene; ds;	
KW	tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24.	
XX		
OS	Mycobacterium tuberculosis.	
OS	Chimeric.	
XX		
Key	Location/Qualifiers	
FT	1. 702	
FT	/*tag= a	
FT	/product= "Mtb24 #1"	
FT	/partial=	
FT	/transl_except= (pos:694. 696, aa:Xaa)	
FT	/note= "No start or stop codon. Xaa= In frame stop codon"	
CDS	2. 702	
FT	/*tag= b	
FT	/product= "Mtb24 #2"	
FT	/partial=	
FT	/note= "No start or stop codon"	
FT	/transl_except= (pos:263. 265, aa:Xaa) /transl_except=	
FT	(pos:353. 355, aa:Xaa) /transl_except= (pos:395. 397,	
FT	aa:Xaa) /transl_except= (pos:470. 472, aa:Xaa)	
FT	/transl_except= (pos:701. 702, aa:Ser)	
FT	/note= "This codon has an apparent 1 nucleotide deletion	
FT	which alters the reading frame. Xaa= In frame stop codon"	
FT	3. 701	
CDS	/*tag= c	
FT	/product= "Mtb24 #3"	
FT	/partial=	
FT	/note= "No start or stop codon"	
FT	/transl_except= (pos:1. 2, aa:Pro) /transl_except=	
FT	(pos:39. 41, aa:Xaa) /transl_except= (pos:321. 323,	
FT	aa:Xaa) /transl_except= (pos:339. 341, aa:Xaa)	
FT	/transl_except= (pos:450. 452, aa:Xaa) /transl_except=	
FT	(pos:621. 623, aa:Xaa)	
FT	/note= "No start or stop codon. Xaa= In frame stop codon"	
XX		
PN	US2002009459-A1.	
XX		
PD	24-JAN-2002.	
XX		
PF	07-APR-1999;	99US-00287849.
XX		
XX	11-MAY-1997.	97US-00A18112.

PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US022058.
XX
PR 11-JUL-2000; 2000US-00614124.
PR 29-AUG-2000; 2000US-00651563.
PR 08-SEP-2000; 2000US-00658824.
PR 26-SEP-2000; 2000US-00671325.
PR 06-OCT-2000; 2000US-00677419.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.
XX
XX (CORI-) CORIXA CORP.
XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb A;
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX
XX WPI; 2002-164634/21.
DR P-PSDB; AAU55587.
XX
XX Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.
XX
XX Example 8; SEQ ID NO 1862; 223pp; English.
XX
XX The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumor protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumor
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumor protein.
CC This sequence encodes a lung tumor associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1-85e-14 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x ABK39769 (1-822)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
DB 22 AGGGCGGTGCGATGAATTCAGCTGTCCAGGTGGCGAGGATTCGCATCCGATC 81

QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGCATGGCATCGCGGCAGATC 111

RESULT 27
ACAI2098
ID ACAI2098 standard; cDNA; 822 BP.
XX
ACAI2098;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human lung cancer protein L801P ORF5/Ra12 fusion protein cDNA.
XX
XX Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
XX T cell expansion; CD4; CD8; RA12; Gene.
XX

OS Homo sapiens.
OS Synthetic.
XX
PN US2002197669-A1.
XX
XX 26-DEC-2002.
XX
XX 03-MAY-2001; 2001US-00849626.
XX
XX 13-DEC-2000; 2000US-00736457.
XX
XX (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
XX
XX Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
PI Clapper JD;
XX
XX WPI; 2003-352750/33.
DR P-PSDB; ABU69562.
XX
XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
PT detecting the presence of lung cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating lung cancer.
XX
XX Example 8; Page; 72pp; English.
XX
XX The invention relates to a polynucleotide encoding a lung tumour protein,
CC comprising a sequence selected from any of the 14 sequences mentioned in
CC the specification, or a sequence (S2) mentioned in specification,
CC complement of S1, sequences consisting of at least 20 contiguous residues
CC of S1, sequences that hybridise to S1, sequences having 75%, preferably
CC 90%, identity to S1, or degenerate variants of S1. Also included are an
CC isolated polypeptide (comprising a sequence (S3) selected from any one of
CC the 4 amino acid sequences mentioned in the specification, a sequence
CC encoded by the polynucleotide, or sequences having at least 70%,
CC preferably 90%, identity to a sequence encoded by the polynucleotide), an
CC expression vector comprising the polynucleotide operably linked to an
CC expression control sequence, a host cell transformed or transfected with
CC the vector, an isolated antibody (or its antigen-binding fragment) that
CC specifically binds to the polypeptide, detecting the presence of a cancer
CC in a patient, a fusion protein comprising the polypeptide, an
CC oligonucleotide that hybridises to S1 under moderately stringent
CC conditions, stimulating and/or expanding T cells specific for a tumour
CC protein (comprising contacting T cells with the polynucleotide, protein
CC or antigen-presenting cells, under conditions and for a time sufficient
CC to permit the stimulation and/or expansion of T cells) and inhibiting the
CC development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T
CC cells isolated from a patient with the polynucleotide, protein or antigen
CC presenting cells that express the polynucleotide, such that T cells
CC proliferate, administering to the patient an effective amount of the
CC proliferated T cells, and thus inhibiting the development of a cancer in
CC the patient. The polynucleotide, protein and cells are useful in a
CC composition for stimulating an immune response in a patient, and for
CC treating a cancer in a patient (particularly lung cancer). The
CC oligonucleotide is useful for determining the presence of a cancer in a
CC patient. The protein and oligonucleotides are useful in pharmaceutical
CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
CC or primer for nucleic acid hybridisation, and in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and proteins in tumour cells. An amplified portion of the
CC polynucleotide is useful for isolating a full-length gene from a suitable
CC library. The present sequence encodes a fusion protein of human RA12 with
CC the protein product of a cDNA (full length, extended or partial) isolated
CC from a library derived from lung tumour/cancer cells. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20020197669
XX

SQ Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.85e-14 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-17 (1-30) x ACA12098 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20

Db 22 ACGGCCGCTCGAATACTCCAGCTGTCCAGGCTGGCGAGGATTCGCCATTCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 28

ACA03284

ID ACA03284 standard; DNA; 822 BP.

XX

AC ACA03284;

XX

DT 22-MAY-2003 (first entry)

XX

DE Lung cancer therapy and diagnosis associated DNA #5.

XX

KW Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ds.

XX

OS Homo sapiens.

XX

PN US2002172952-A1.

XX

PD 21-NOV-2002.

XX

PF 10-JUL-2001; 2001US-00902941.

XX

PR 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419336.

PR 17-DEC-1999; 99US-00466887.

PR 30-DEC-1999; 99US-00476300.

PR 06-MAR-2000; 2000US-00519642.

PR 22-MAR-2000; 2000US-00533077.

PR 10-APR-2000; 2000US-00546259.

PR 27-APR-2000; 2000US-00560406.

PR 05-JUN-2000; 2000US-00569184.

PR 11-JUL-2000; 2000US-00614124.

PR 29-AUG-2000; 2000US-00651563.

PR 08-SEP-2000; 2000US-00658824.

PR 26-SEP-2000; 2000US-00671325.

PR 06-OCT-2000; 2000US-00677419.

PR 30-OCT-2000; 2000US-00702705.

PR 13-DEC-2000; 2000US-00736457.

PR 03-MAY-2001; 2001US-00849626.

XX

PA (CORI-) CORIXA CORP.

XX

PI Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;

PI Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;

XX

DR WPI; 2003-328427/31.

XX

PT New polynucleotide, useful for preparing a composition for treating or

PT inhibiting development of cancer, e.g. lung cancer.

XX

PS Example 8; SEQID NO 1862; 82pp; English.

XX

CC The invention describes an isolated polynucleotide comprising one of 32

CC sequences, complement or degenerate variants of them. The polynucleotide

CC is useful for preparing a composition e.g. a vaccine or for gene therapy.

CC

CC for treating or inhibiting development of cancer, e.g. lung cancer. This

CC sequence represents a polynucleotide associated with the compositions and

CC methods for the therapy and diagnosis of lung cancer

XX

SQ Sequence 822 BP; 146 A; 281 C; 270 G; 125 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.85e-14 Length: 822
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-17 (1-30) x ACA03284 (1-822)

Qy 1 ThrAlaAlaSerAspAsnPhcGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProfile 20

Db 22 ACGGCCGCTCGAATACTCCAGCTGTCCAGGCTGGCGAGGATTCGCCATTCGATC 81

Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30

Db 82 GGGCAGGCGATGGCGATCGCGGCCAGATC 111

RESULT 29

ABK39776

ID ABK39776 standard; cDNA; 861 BP.

XX

AC ABK39776;

XX

DT 21-MAY-2002 (first entry)

XX

DE DNA encoding Ral28-L985P fusion protein.

XX

KW Lung tumour; cancer; T cell; immune response stimulator; cytostatic;

XX

OS gene; ss.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

PN WO200204514-A2.

XX

PD 17-JAN-2002.

XX

PF 10-JUL-2001; 2001WO-US022058.

XX

PR 11-JUL-2000; 2000US-00614124.

PR 29-AUG-2000; 2000US-00651563.

PR 08-SEP-2000; 2000US-00658824.

PR 26-SEP-2000; 2000US-00671325.

PR 06-OCT-2000; 2000US-00677419.

PR 30-OCT-2000; 2000US-00702705.

PR 13-DEC-2000; 2000US-00736457.

PR 03-MAY-2001; 2001US-00849626.

XX

PA (CORI-) CORIXA CORP.

XX

PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;

PI Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;

XX

XX Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;

XX WPI; 2002-164634/21.

XX P-PSDB; AAU85594.

XX

PT Novel polynucleotide encoding a lung tumor polypeptide useful for

PT stimulating and/or expanding T cells specific for a tumor protein.

XX

PS Claim 1; SEQ ID NO 1877; 223pp; English.

XX

CC The invention describes an isolated polynucleotide and polypeptide useful

CC for stimulating and/or expanding T cells specific for a tumor protein

CC for determining the presence of a cancer in a patient. A composition

CC containing the polynucleotide and/or polypeptide is useful for treating a

CC lung cancer in a patient. The polypeptide is useful for removing tumour
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumour protein.
CC This sequence encodes a lung tumour associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 861 BP; 186 A; 244 C; 209 G; 222 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.96e-14 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-684-215B-17 (1-30) x ABK39776 (1-861)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
DB 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGTGGCGAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGATGGCGATCGCGGCCAGATC 111

RESULT 30

ACAL12105

ID ACAL12105 standard; cDNA; 861 BP.

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

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XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

XX ACAL12105;

CC The invention relates to a polynucleotide encoding a lung tumour protein,
CC comprising a sequence selected from any of the 14 sequences mentioned in
CC the specification, or a sequence (82) mentioned in specification,
CC complement of S1, sequences consisting of at least 20 contiguous residues
CC of S1, sequences that hybridise to S1, sequences having 75%, preferably
CC 90%, identity to S1, or degenerate variants of S1. Also included are an
CC isolated polypeptide (comprising a sequence (S3) selected from any one of
CC the 4 amino acid sequences mentioned in the specification, a sequence
CC encoded by the polynucleotide, or sequences having at least 70%,
CC preferably 90%, identity to a sequence encoded by the polynucleotide), an
CC expression vector comprising the polynucleotide operably linked to an
CC expression control sequence, a host cell transformed or transfected with
CC the vector, an isolated antibody (or its antigen-binding fragment) that
CC specifically binds to the polypeptide, detecting the presence of a cancer
CC in a patient, a fusion protein comprising the polypeptide, an
CC oligonucleotide that hybridises to S1 under moderately stringent
CC conditions, stimulating and/or expanding T cells specific for a tumour
CC protein (comprising contacting T cells with the polynucleotide, protein
CC or antigen-presenting cells, under conditions and for a time sufficient
CC to permit the stimulation and/or expansion of T cells) and inhibiting the
CC development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T
CC cells isolated from a patient with the polynucleotide, protein or antigen
CC presenting cells that express the polynucleotide, such that T cells
CC proliferate, administering to the patient an effective amount of the
CC proliferated T cells, and thus inhibiting the development of a cancer in
CC the patient. The polynucleotide, protein and cells are useful in a
CC composition for stimulating an immune response in a patient, and for
CC treating a cancer in a patient (particularly lung cancer). The
CC oligonucleotide is useful for determining the presence of a cancer in a
CC patient. The protein and oligonucleotides are useful in pharmaceutical
CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
CC or primer for nucleic acid hybridisation, and in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and proteins in tumour cells. An amplified portion of the
CC polynucleotide is useful for isolating a full-length gene from a suitable
CC library. The present sequence encodes a fusion protein of human RA12 with
CC the protein product of a cDNA (full length, extended or partial) isolated
CC from a library derived from lung tumour/cancer cells. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20020197669

XX Sequence 861 BP; 186 A; 244 C; 209 G; 222 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.96e-14 Length: 861
Score: 148.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-684-215B-17 (1-30) x ACAL12105 (1-861)

QY 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProile 20
DB 22 ACGGCGCGTCCGATTAATTCAGCTGTCCAGGTGGCGAGGATTCGCCATTCGATC 81
QY 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
DB 82 GGGCAGCGATGGCGATCGCGGCCAGATC 111

Search completed: April 29, 2004, 23:03:07
Job time : 90.3349 secs

XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
XX detecting the presence of lung cancer in a patient, and in pharmaceutical
XX compositions, e.g. vaccines, for treating lung cancer.

XX Example 10; Page; 72pp; English.